

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 30, 2004, 14:42:40 ; Search time 15 Seconds
(without alignments)

577.301 Million cell updates/sec

Title: US-09-997-653-377

Perfect score: 462

Sequence: 1 MTFFLSLILLIVCEAIWRSN.....DSRGLILGAEWGRVKKNT 90

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

PIR 79.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	70	15.2	256	AE1734	anti-repressor hom
2	68.5	14.8	495	S76957	hypothetical prote
3	68.5	14.8	622	A34549	transferrin recept
4	68	14.7	280	E82099	phosphatidate cyti
5	66.5	14.7	1334	T41524	rho1 gdp-gtp excha
6	66.5	14.4	337	A83026	hypothetical prote
7	66.5	14.4	479	S41015	transcription fact
8	66	14.3	851	T47495	hypothetical prote
9	65	14.1	313	A82436	transcription regu
10	65	14.1	360	H97313	protein distantly
11	65	14.1	368	S36576	E2 protein - human
12	65	14.1	379	T24654	hypothetical prote
13	64.5	14.0	532	T06029	hypothetical prote
14	64	13.9	257	AI1442	hypothetical prote
15	64	13.9	430	T46099	anti-repressor (Ba
16	64	13.9	548	T28910	hypothetical prote
17	63.5	13.7	598	A64594	hypothetical prote
18	63.5	13.7	651	A96781	site-specific DNA-
19	63.5	13.7	669	I54205	unknown protein F9
20	63.5	13.7	705	T48144	galactosylceramida
21	63.5	13.7	850	T14472	protein kinase CDC
22	63.5	13.7	882	S57704	S-receptor kinase
23	63	13.6	249	T00169	hypothetical prote
24	63	13.6	250	H89989	anti repressor - S
25	63	13.6	441	F86185	hypothetical prote
26	63	13.6	457	E96572	hypothetical prote
27	63	13.6	2425	D69426	surface layer prot
28	62.5	13.5	379	S76029	hypothetical prote
29	62.5	13.5	381	T19402	hypothetical prote

30	62.5	13.5	617	2	AE2897	conserved hypothet
31	62.5	13.5	641	2	H97672	hypothetical prote
32	62.5	13.5	849	1	S51527	S-receptor kinase
33	62.5	13.5	1123	2	AD2045	hypothetical prote
34	62.5	13.5	1553	2	TI18502	hypothetical prote
35	62	13.4	84	2	F81128	probable lipoprote
36	62	13.4	149	2	S76835	hypothetical prote
37	62	13.4	613	2	A88448	protein C45G9.6 (i
38	62	13.4	1017	2	T30542	major surface glyc
39	62	13.4	1022	2	T30543	major surface glyc
40	62	13.4	1634	2	E64410	DNA-directed DNA p
41	61.5	13.3	409	2	H72669	probable N2,N2-dim
42	61.5	13.3	500	2	S22458	cellulase (EC 3.2.
43	61.5	13.3	516	2	S28060	serum response fac
44	61.5	13.3	668	2	C96501	hypothetical prote
45	61.5	13.3	887	2	T39452	conserved hypothet
46	61.5	13.3	960	2	S54461	hypothetical prote
47	61.5	13.3	4868	2	B54161	ryanodine-binding
48	61	13.2	229	2	T36659	probable transposa
49	61	13.2	237	1	A36056	tumor-associated a
50	61	13.2	279	2	T36998	probable transposa
51	61	13.2	415	2	I53040	beta-2 adrenergic
52	61	13.2	561	2	C84721	hypothetical prote
53	61	13.2	790	2	S61587	transcription acti
54	61	13.2	1774	2	S13178	6-methylsalicylic
55	61	13.2	1801	2	T26774	hypothetical prote
56	60.5	13.1	221	2	A64567	thiol-disulfide in
57	60.5	13.1	222	2	F96759	probable tumor-rel
58	60.5	13.1	410	2	E72316	hypothetical prote
59	60.5	13.1	567	2	JN0459	transforming growt
60	60.5	13.1	572	2	F90564	conserved hypothet
61	60.5	13.1	600	2	A38091	calpastatin, long
62	60.5	13.1	654	2	T50198	probable transcrip
63	60.5	13.1	676	2	S61977	transcription fact
64	60.5	13.1	1231	2	A86359	hypothetical prote
65	60.5	13.1	1272	2	S26180	neurofascin - chic
66	60	13.0	312	2	D81163	penicillin-binding
67	60	13.0	312	2	A81943	probable D-alanyl-
68	60	13.0	358	2	AC1345	oxidoreductase hom
69	60	13.0	486	2	B84914	hypothetical prote
70	60	13.0	514	2	B96653	hypothetical prote
71	60	13.0	604	2	S52706	probable membrane
72	60	13.0	605	2	A96660	protein F2K11.20 (
73	60	13.0	671	2	A56592	NADPH-ferrhemopro
74	60	13.0	1039	2	AI0422	probable integral
75	59.5	12.9	200	2	H82318	conserved hypothet
76	59.5	12.9	374	2	A84783	hypothetical prote
77	59.5	12.9	565	2	T33851	thin filament-asso
78	59.5	12.9	663	2	A97066	transketolase, TKT
79	59	12.8	82	2	F97043	hypothetical prote
80	59	12.8	102	2	G70065	hypothetical prote
81	59	12.8	229	2	T29310	hypothetical prote
82	59	12.8	278	2	A83689	hypothetical prote
83	59	12.8	399	2	B83398	hypothetical prote
84	59	12.8	474	2	A57480	tubulointerstitial
85	59	12.8	499	2	S70113	hypothetical prote
86	59	12.8	641	2	T07668	hypothetical prote
87	59	12.8	708	2	S62907	starch synthase (E
88	59	12.8	793	2	S73662	gelatinase B (EC 3
89	59	12.8	970	2	S48485	probable lipoprote
90	59	12.8	1084	2	T31173	transcription acti
91	59	12.8	1116	2	T38073	RNA-directed DNA p
92	59	12.8	1804	2	H96597	serine/threonine-p
93	58.5	12.7	155	2	G82230	hypothetical prote
94	58.5	12.7	223	2	A71863	conserved hypothet
95	58.5	12.7	371	2	T49786	hypothetical prote
96	58.5	12.7	387	2	AI2569	hypothetical prote
97	58.5	12.7	418	2	T47239	oxalate/formate an
98	58.5	12.7	439	2	I39524	probable porin - A
99	58.5	12.7	466	2	B97030	lps glycosyltransf
100	58.5	12.7	531	2	S57752	hal3 protein - Yea
101	58.5	12.7	532	2	A84493	probable Achilare
102	58.5	12.7	542	2	F64424	Chaperonin - Metha

103	58.5	12.7	559	2	T37761	hypothetical prote	176	56.5	12.2	274	2	H72521	probable thiazole
104	58.5	12.7	561	2	C96837	nodulin-like prote	177	56.5	12.2	281	2	A12078	hypothetical prote
105	58.5	12.7	579	2	T02574	hypothetical prote	178	56.5	12.2	325	2	E82704	lipase XF1253 [imp
106	58.5	12.7	613	2	T24662	hypothetical prote	179	56.5	12.2	334	2	T50816	probable transcript
107	58.5	12.7	953	1	B30169	leukotoxin A - Pas	180	56.5	12.2	338	2	T41021	ser-thr protein ki
108	58.5	12.7	955	1	A35254	leukotoxin A - Pas	181	56.5	12.2	414	2	A69907	cell wall-binding
109	58.5	12.7	1008	2	T18832	probable RNA helic	182	56.5	12.2	418	2	T25041	hypothetical prote
110	58.5	12.7	1701	2	A26868	major merozoite su	183	56.5	12.2	490	2	T49616	hypothetical prote
111	58.5	12.7	1701	2	A26868	major merozoite su	184	56.5	12.2	500	2	AD1047	probable amino aci
112	58.5	12.7	1726	1	SAZQGM	major merozoite su	185	56.5	12.2	538	2	H86329	transferrin recept
113	58.5	12.7	1726	1	A45948	major merozoite su	186	56.5	12.2	776	2	E90591	lipoprotein [impor
114	58.5	12.7	3345	2	T13423	hypothetical prote	187	56.5	12.2	776	2	E90591	probable nitrogen
115	58	12.6	211	2	F64218	ribosomal protein	188	56.5	12.2	855	2	T41336	probable protein pr
116	58	12.6	260	2	F98909	hypothetical prote	189	56.5	12.2	1099	2	T14850	S-layer protein p
117	58	12.6	270	2	H83327	exodeoxyribonucle	190	56.5	12.2	1333	2	S65812	RNA-directed DNA p
118	58	12.6	288	2	F70244	antigen, P35 homol	191	56.5	12.2	1422	2	T24212	hypothetical prote
119	58	12.6	439	2	H70250	hypothetical prote	192	56.5	12.2	1428	1	IS8Y12	DNA topoisomerase
120	58	12.6	488	2	H86658	N-acetylmuramoyl-L	193	56	12.1	70	2	T44130	hypothetical prote
121	58	12.6	439	2	H86658	genome polyprotein	194	56	12.1	160	2	JR0136	lectin precursor -
122	58	12.6	453	2	A48348	hypothetical prote	195	56	12.1	160	2	AH2342	hypothetical prote
123	58	12.6	538	2	E96492	serine/threonine k	196	56	12.1	187	2	T37399	20K virion protein
124	58	12.6	642	2	AE2407	pyruvate-formate l	197	56	12.1	192	2	E42518	A12L protein - vac
125	58	12.6	743	2	A97021	hypothetical prote	198	56	12.1	196	2	E86736	peptidyl-brolyl ci
126	58	12.6	778	2	T22234	hypothetical prote	199	56	12.1	205	2	T46434	hypothetical prote
127	58	12.6	836	2	AD2565	hypothetical prote	200	56	12.1	289	2	T42994	conserved hypothet
128	58	12.6	933	1	OPHUIT	iodide peroxidase	201	56	12.1	292	2	T40045	conserved hypothet
129	58	12.6	938	2	T51422	hypothetical prote	202	56	12.1	305	2	A69690	ribose ABC transpo
130	58	12.6	1265	2	T45788	probable disease r	203	56	12.1	323	2	A72059	conserved hypothet
131	58	12.6	1616	2	JC6510	ras-responsive ele	204	56	12.1	323	2	H86564	CT476 hypothetical
132	58	12.6	2526	2	T20531	hypothetical prote	205	56	12.1	362	2	S68471	asparaginase (EC 3
133	58	12.6	2722	2	T20532	hypothetical prote	206	56	12.1	371	2	C70237	hypothetical prote
134	58	12.6	2738	2	E88320	protein F07A11.6 [207	56	12.1	428	2	F81694	pyruvate dehydroge
135	57.5	12.4	6420	2	T30283	polyketide synthas	208	56	12.1	448	2	F81703	phospholipase D fa
136	57.5	12.4	141	2	H82220	hypothetical prote	209	56	12.1	461	2	C98120	hypothetical prote
137	57.5	12.4	246	2	H97922	glutamine ABC tran	210	56	12.1	461	2	C98120	glycerol-3-phospha
138	57.5	12.4	246	2	D95052	amino acid ABC tra	211	56	12.1	476	2	JC7189	tubulointerstitial
139	57.5	12.4	329	2	E84515	proline iminopepti	212	56	12.1	556	2	T28960	hypothetical prote
140	57.5	12.4	353	2	AB9897	protein C5OH11.4 [213	56	12.1	587	2	T00316	toxA-regulated lip
141	57.5	12.4	412	2	A48702	2-methyl-branched-	214	56	12.1	608	2	S32823	somatotropin recep
142	57.5	12.4	412	2	C96789	protein T23E18.6 [215	56	12.1	622	2	C95255	hypothetical prote
143	57.5	12.4	452	2	C90044	hypothetical prote	216	56	12.1	622	2	T49426	Type 2C Protein Ph
144	57.5	12.4	491	1	FGHUB	hypothetical prote	217	56	12.1	631	2	D96683	hypothetical prote
145	57.5	12.4	501	2	AH1852	fibrogen beta ch	218	56	12.1	712	2	H97555	DNA gyrase chain b
146	57.5	12.4	533	2	S10841	hypothetical prote	219	56	12.1	712	2	A87776	protein C01G5.6 [i
147	57.5	12.4	553	2	S22954	gene ND5 intron 1	220	56	12.1	856	2	A89711	hypothetical prote
148	57.5	12.4	651	2	S47282	finger protein zfp	221	56	12.1	923	2	S50482	hypothetical prote
149	57.5	12.4	751	1	WMXRGB	merozoite surface	222	56	12.1	960	2	T00808	HIV-1 retropepsin
150	57.5	12.4	752	2	G96510	probable core prot	223	56	12.1	1036	1	GNLJG2	phosphatidylserine
151	57.5	12.4	854	1	QRHYLD	hypothetical prote	224	56	12.1	1138	2	S64484	hypothetical prote
152	57.5	12.4	869	2	T44440	LDL receptor precu	225	56	12.1	1184	2	A96638	IGA-specific serin
153	57.5	12.4	1121	2	T47970	chitinase (EC 3.2.	226	56	12.1	1394	2	S60762	hypothetical prote
154	57.5	12.4	1944	2	T40065	tRNA-splicing endo	227	56	12.1	1419	2	T32970	EGF repeat transme
155	57	12.3	93	2	A41975	major histocompati	228	56	12.1	1687	2	T30176	ychN protein homol
156	57	12.3	158	2	G95186	hypothetical prote	229	55.5	12.0	114	1	E64423	nodule specific pr
157	57	12.3	158	2	H98053	hypothetical prote	230	55.5	12.0	168	2	T09333	hypothetical prote
158	57	12.3	186	1	G64005	hypothetical prote	231	55.5	12.0	248	2	T33230	hypothetical prote
159	57	12.3	266	2	A12289	hypothetical prote	232	55.5	12.0	283	2	F96926	cell division inhi
160	57	12.3	302	2	B96921	probable sugar pho	233	55.5	12.0	298	2	C82824	lectin M-ASGP-BP p
161	57	12.3	323	2	AC3514	hypothetical cytos	234	55.5	12.0	306	2	A42230	probable transcript
162	57	12.3	491	2	A69123	biotin carboxylase	235	55.5	12.0	308	2	C83586	hypothetical prote
163	57	12.3	506	2	F64862	hypothetical prote	236	55.5	12.0	370	2	G98266	hypothetical prote
164	57	12.3	569	2	C69422	hydrogenase (EC 1.	237	55.5	12.0	437	2	T30897	transcription fact
165	57	12.3	569	2	AB0005	probable exported	238	55.5	12.0	479	1	TVCHE2	nuclear protein fk
166	57	12.3	645	2	B98983	conserved hypothet	239	55.5	12.0	510	2	A32380	replication protei
167	57	12.3	704	2	S25586	lcrD protein - Yer	240	55.5	12.0	616	1	A40457	methyl-accepting c
168	57	12.3	804	2	T32864	hypothetical prote	241	55.5	12.0	754	2	AF2849	hypothetical prote
169	57	12.3	814	2	T47641	hypothetical prote	242	55.5	12.0	768	2	D97626	glycoprotein phosp
170	57	12.3	898	2	T42131	probable toxR-regu	243	55.5	12.0	839	2	A56337	outer membrane ush
171	57	12.3	1070	2	AI0484	probable autotrans	244	55.5	12.0	842	1	C56271	probable S-recepto
172	57	12.3	2109	2	T17490	polyketide synthas	245	55.5	12.0	857	2	T14471	hypothetical prote
173	56.5	12.2	207	2	C71449	hypothetical prote	246	55.5	12.0	884	2	E86244	unknown protein, 4
174	56.5	12.2	209	2	T29765	hypothetical prote	247	55.5	12.0	955	2	T14361	H+-exporting ATPas
175	56.5	12.2	212	2	D96610	probable integral	248	55.5	12.0				
			254	2	S48547	probable membrane							

249	55.5	12.0	965	2	T50670	actin bundling pro	322	54.5	11.8	764	2	C98117	conserved hypothet
250	55.5	12.0	1030	2	T18374	B-cell receptor pr	323	54.5	11.8	765	2	E98254	hypothetical prote
251	55.5	12.0	1035	2	T30287	exo-alpha-sialidas	324	54.5	11.8	797	2	C96313	F2H15.5 protein -
252	55.5	12.0	1035	2	G98063	exo-alpha-sialidas	325	54.5	11.8	819	2	B95136	conserved domain p
253	55.5	12.0	1225	2	T16346	hypothetical prote	326	54.5	11.8	832	1	S27754	S-receptor kinase
254	55.5	12.0	1520	2	AF3008	polyketide synthas	327	54.5	11.8	839	2	G95115	conserved hypothet
255	55.5	12.0	1520	2	G98275	hypothetical prote	328	54.5	11.8	853	2	C97985	hypothetical prote
256	55.5	12.0	2529	2	A56923	transcription fact	329	54.5	11.8	892	2	T09193	ataxin 7 - human
257	55.5	12.0	2578	2	A56923	transcription fact	330	54.5	11.8	1046	2	S67786	hypothetical prote
258	55.5	12.0	4660	2	T42737	gp330 protein prec	331	54.5	11.8	1094	2	T05472	hypothetical prote
259	55	11.9	135	2	C90360	conserved hypothet	332	54.5	11.8	1375	2	T42586	major capsid prote
260	55	11.9	157	2	S19735	lectin precursor -	333	54.5	11.8	1436	2	S57238	forked protein 5.4
261	55	11.9	201	2	J01940	hypothetical 23K p	334	54.5	11.8	1449	2	S57237	major merozoite su
262	55	11.9	212	2	S66410	hypothetical prote	335	54.5	11.8	1631	1	SAZQK1	probable major sur
263	55	11.9	231	2	T02585	hypothetical prote	336	54.5	11.8	1639	2	S05603	CD339 protein - ye
264	55	11.9	295	2	E82659	peptidyl-prolyl ci	337	54.5	11.8	2108	2	S28417	peptide synthetase
265	55	11.9	314	2	G86869	hypothetical prote	338	54.5	11.8	3603	1	D69681	hypothetical prote
266	55	11.9	327	2	A82335	conserved hypothet	339	54.5	11.8	6713	2	B89921	hypothetical 7.6K
267	55	11.9	335	2	A01686	peptidase homolog	340	54.5	11.8	68	2	J02006	mannose-binding le
268	55	11.9	364	2	H50331	hypothetical prote	341	54	11.7	183	2	S62650	hypothetical prote
269	55	11.9	369	2	S20811	proteoglycan I - m	342	54	11.7	201	2	S54475	hypothetical prote
270	55	11.9	385	2	A84696	probable zinc tran	343	54	11.7	231	1	G84941	hypothetical prote
271	55	11.9	402	2	G83021	probable acyl-CoA	344	54	11.7	241	2	T26676	hypothetical prote
272	55	11.9	507	2	D64083	adenylosuccinate l	345	54	11.7	253	2	T06113	hypothetical prote
273	55	11.9	546	2	B75573	conserved hypothet	346	54	11.7	258	2	I56220	tryptase 2 - rat
274	55	11.9	562	2	T80899	furostanol glycosi	347	54	11.7	258	2	S69541	hypothetical prote
275	55	11.9	578	2	T30971	hypothetical prote	348	54	11.7	259	2	T09317	hypothetical prote
276	55	11.9	590	2	S63193	hypothetical prote	349	54	11.7	322	2	H85474	glycoprotein - hum
277	55	11.9	624	2	S44938	nitrogen permease	350	54	11.7	340	2	AE0129	UDP-3-O-[3-hydroxy
278	55	11.9	651	2	T12083	beta-fructofuranos	351	54	11.7	347	2	H91044	hypothetical prote
279	55	11.9	660	2	E81839	probable transmemb	352	54	11.7	347	2	C85889	hypothetical prote
280	55	11.9	665	2	P97032	beta-glucosidase f	353	54	11.7	347	2	A65022	hypothetical prote
281	55	11.9	675	2	E81101	transporter, BCCR	354	54	11.7	359	2	B84080	multiple sugar tra
282	55	11.9	704	2	A41321	low calcium respon	355	54	11.7	361	2	S57895	hypothetical prote
283	55	11.9	735	2	T50068	probable ATP-depen	356	54	11.7	367	2	T10088	uroporphyrinogen d
284	55	11.9	863	2	AE0525	outer membrane ush	357	54	11.7	392	2	G75452	probable glutamate
285	55	11.9	883	2	B85725	probable fibrial	358	54	11.7	397	2	T05286	hypothetical prote
286	55	11.9	1117	2	T13727	hypothetical prote	359	54	11.7	412	2	C82522	type I restriction
287	55	11.9	1240	2	S52734	hypothetical prote	360	54	11.7	422	2	G72227	hypothetical prote
288	55	11.9	1448	2	A12007	Subtilase family p	361	54	11.7	436	2	B75069	hypothetical prote
289	55	11.9	2273	2	T09083	hemagglutinin/hemo	362	54	11.7	481	2	S56299	phosphoglycerate m
290	55	11.9	10797	2	T30192	probable peptide s	363	54	11.7	488	2	T09138	ARS-binding protei
291	54.5	11.8	112	2	B12700	conserved hypothet	364	54	11.7	496	2	S33791	nucleoprotein - in
292	54.5	11.8	169	2	B97483	hypothetical prote	365	54	11.7	498	1	VHIV61	spike glycoprotein
293	54.5	11.8	216	2	A14441	hypothetical prote	366	54	11.7	524	1	VGPNRV	hypothetical prote
294	54.5	11.8	231	2	A86212	hypothetical prote	367	54	11.7	528	2	T31905	cobalamin biosynth
295	54.5	11.8	257	2	D87152	conserved hypothet	368	54	11.7	533	2	G69140	hypothetical prote
296	54.5	11.8	268	2	B64236	protoporphyrin IX	369	54	11.7	552	2	T30972	two-component sens
297	54.5	11.8	307	2	H83660	cysteine synthase	370	54	11.7	619	2	AH2244	finger protein MSN
298	54.5	11.8	319	2	T43040	hypothetical prote	371	54	11.7	630	1	S37884	conserved hypothet
299	54.5	11.8	321	2	E90492	hypothetical prote	372	54	11.7	648	2	AD3070	hypothetical prote
300	54.5	11.8	328	2	G86263	hypothetical prote	373	54	11.7	653	2	E98216	Rab geranylgeranyl
301	54.5	11.8	354	2	S29718	gene nodal protein	374	54	11.7	654	2	I37234	hypothetical prote
302	54.5	11.8	364	2	S43574	C05B5.3 protein (c	375	54	11.7	654	2	T19785	methyl-accepting c
303	54.5	11.8	401	2	C88571	protein C05B5.3 [i	376	54	11.7	662	2	D54078	transketolase homo
304	54.5	11.8	434	2	T34350	hypothetical prote	377	54	11.7	664	2	AF11237	transketolase homo
305	54.5	11.8	459	2	G90558	aminopeptidase (le	378	54	11.7	664	2	AF1600	protein C17G10.4c
306	54.5	11.8	470	2	E88130	protein F10G7.5 [i	379	54	11.7	681	2	E88158	hypothetical prote
307	54.5	11.8	510	2	D69946	phage-related prot	380	54	11.7	706	2	A96576	gelatinase B (EC 3
308	54.5	11.8	519	2	I56566	nicotinic acetylch	381	54	11.7	707	1	A34458	hypothetical prote
309	54.5	11.8	521	2	I51693	XPolycomb - Africa	382	54	11.7	708	2	T34098	hypothetical prote
310	54.5	11.8	524	2	S33840	homeotic protein s	383	54	11.7	747	2	A71440	hypothetical prote
311	54.5	11.8	547	2	E96530	Similar to CCS1 [i	384	54	11.7	761	2	S60992	outer membrane pro
312	54.5	11.8	592	2	D69754	prophage p12 prote	385	54	11.7	803	2	AB0530	hypothetical prote
313	54.5	11.8	592	2	G69159	sensory transducti	386	54	11.7	810	2	A64742	hypothetical prote
314	54.5	11.8	592	2	S51371	transforming growt	387	54	11.7	810	2	C90651	hypothetical prote
315	54.5	11.8	668	2	C71868	hypothetical prote	388	54	11.7	810	2	C85502	S-receptor kinase
316	54.5	11.8	677	2	W37398	MG260 homolog H91	389	54	11.7	854	2	T14377	pyruvate dehydroge
317	54.5	11.8	699	2	AB3031	conserved hypothet	390	54	11.7	882	2	G83018	protein T24P13.14
318	54.5	11.8	738	2	S37876	glutamine-rich pro	391	54	11.7	969	2	C86394	COP1-interacting p
319	54.5	11.8	740	2	H82807	beta-glucosidase X	392	54	11.7	1058	2	T08935	probable protein-t
320	54.5	11.8	764	1	S67561	protein kinase RPK	393	54	11.7	1063	2	T34097	
321	54.5	11.8	764	2	E95252	Conserved hypothet	394	54	11.7				

395	54	11.7	1148	2	S51855	hypothetical prote	468	53	11.5	336	1	PRASAK	glutamyl endopepti
396	54	11.7	1184	2	T41515	coiled coil protei	469	53	11.5	342	2	G89873	hypothetical prote
397	54	11.7	1301	2	T07321	DNA-directed RNA p	470	53	11.5	368	2	G82870	GTP-binding protei
398	54	11.7	1425	2	T22433	hypothetical prote	471	53	11.5	398	1	D64464	hypothetical prote
399	54	11.7	2256	2	A80018	large repetitive p	472	53	11.5	416	1	A41267	transcription fact
400	54	11.7	3295	2	AB0074	probable adhesin Y	473	53	11.5	436	2	G72299	conserved hypotet
401	54	11.7	3381	2	T42389	versican precursor	474	53	11.5	454	2	T26296	hypothetical prote
402	53.5	11.6	99	2	T10554	hypothetical prote	475	53	11.5	457	2	JC4541	NADH oxidase (H2O-
403	53.5	11.6	121	2	T09469	hypothetical prote	476	53	11.5	462	2	A75435	protoporphyrinogen
404	53.5	11.6	126	2	J05341	repressor protein	477	53	11.5	464	2	T39699	glutathione-disulf
405	53.5	11.6	221	2	F97818	hypothetical prote	478	53	11.5	498	1	VHIVX2	nucleoprotein - in
406	53.5	11.6	242	2	S63641	hypothetical prote	479	53	11.5	498	1	VHIVX3	nucleoprotein - in
407	53.5	11.6	262	2	A12480	transposase alr702	480	53	11.5	498	1	VHIVX4	nucleoprotein - in
408	53.5	11.6	279	2	S73526	probable lipoprote	481	53	11.5	504	2	A23282	RAD52 protein - ye
409	53.5	11.6	285	2	AD0613	probable format t	482	53	11.5	520	2	C81424	cytochrome bd oxid
410	53.5	11.6	285	2	A32305	probable format t	483	53	11.5	531	2	T51922	hypothetical prote
411	53.5	11.6	285	2	S90752	probable format t	484	53	11.5	535	2	S68446	origin recognition
412	53.5	11.6	285	2	A85616	probable format t	485	53	11.5	560	2	T16562	hypothetical prote
413	53.5	11.6	318	2	T22996	hypothetical prote	486	53	11.5	575	2	S46329	intermediate filam
414	53.5	11.6	328	2	S27536	epsilon-toxin - Cl	487	53	11.5	587	2	A10180	conserved hypotet
415	53.5	11.6	328	2	A87410	myo-inositol 2-deh	488	53	11.5	593	2	A72221	conserved hypotet
416	53.5	11.6	355	2	T52265	nitrilase (EC 3.5.	489	53	11.5	596	1	RRNZB3	polymerase-associa
417	53.5	11.6	368	1	EGHUN	biglycan precursor	490	53	11.5	611	2	T22855	hypothetical prote
418	53.5	11.6	377	2	T12185	transcriptional fact	491	53	11.5	631	2	T32761	hypothetical prote
419	53.5	11.6	381	2	C90543	hypothetical prote	492	53	11.5	634	2	T00359	hypothetical prote
420	53.5	11.6	404	2	T50335	mating pheromone r	493	53	11.5	638	2	T28932	probable 4-coumara
421	53.5	11.6	411	2	PC2060	genome polyprotein	494	53	11.5	644	2	T24366	hypothetical prote
422	53.5	11.6	436	2	AB2417	hypothetical prote	495	53	11.5	677	2	T45921	probable G-protein
423	53.5	11.6	442	2	C70135	flagellar hook pro	496	53	11.5	731	2	E98099	peptidoglycan glyc
424	53.5	11.6	449	2	I64246	ATP-dependent RNA	497	53	11.5	743	2	T42557	tegument protein 1
425	53.5	11.6	449	2	G95876	probable permease	498	53	11.5	772	2	T06154	hypothetical prote
426	53.5	11.6	453	2	S74805	DNA photolyase - S	499	53	11.5	798	2	T33022	hypothetical prote
427	53.5	11.6	458	2	D70410	cytosolic axial fi	500	53	11.5	848	2	E86443	probable outer mem
428	53.5	11.6	496	2	B97519	glutamyl-tRNA(gln)	501	53	11.5	866	1	C64834	probable G-protein
429	53.5	11.6	510	2	A64595	flagellin A - Heli	502	53	11.5	899	2	S51341	sericinB - silkwo
430	53.5	11.6	517	2	D68804	sensor protein kin	503	53	11.5	915	2	S74283	probable protein k
431	53.5	11.6	558	2	AD1349	pheromone ABC tran	504	53	11.5	947	2	H84866	hypothetical prote
432	53.5	11.6	576	1	S22453	colicin E7 (EC 3.1	505	53	11.5	960	2	T50383	homolog to yeast c
433	53.5	11.6	609	1	A43458	replication protei	506	53	11.5	984	2	A55137	hyaluronate lyase
434	53.5	11.6	647	2	S26396	transcription fact	507	53	11.5	1055	2	S53092	pol polyprotein -
435	53.5	11.6	663	2	S51865	Rgp1 protein - yea	508	53	11.5	1163	2	A36685	205K microtubule-a
436	53.5	11.6	677	2	H84382	heterodisulfide re	509	53	11.5	1217	2	S52714	sericinB - silkwo
437	53.5	11.6	687	2	S56939	probable membrane	510	53	11.5	1233	2	T14157	serine/threonine p
438	53.5	11.6	698	2	S49206	GI cyclin CLN1 - Y	511	53	11.5	1274	2	S59405	probable membrane
439	53.5	11.6	761	2	JC5759	brain-specific ser	512	53	11.5	1450	2	S78060	probable DNA-direc
440	53.5	11.6	831	2	A99304	pancillin acylase	513	53	11.5	1505	2	T31418	synaptonemal compl
441	53.5	11.6	872	2	S49538	CocC protein precu	514	53	11.5	1505	2	T00327	hypothetical prote
442	53.5	11.6	872	2	H86471	hypothetical prote	515	53	11.5	1505	2	T31418	hypothetical prote
443	53.5	11.6	887	2	B84954	pyruvate dehydroge	516	53	11.5	1505	2	T00327	hypothetical prote
444	53.5	11.6	929	2	G72677	hypothetical prote	517	53	11.5	1505	2	T00327	hypothetical prote
445	53.5	11.6	993	2	G84632	hypothetical prote	518	53	11.5	1505	2	T00327	hypothetical prote
446	53.5	11.6	1023	1	LEBAC	hemolysin A - Esch	519	53	11.4	1505	2	T00327	hypothetical prote
447	53.5	11.6	1024	2	S10056	hemolysin A - Esch	520	53	11.4	1505	2	T00327	hypothetical prote
448	53.5	11.6	1138	2	H84529	probable rhoI GDP-	521	53	11.4	1505	2	T00327	hypothetical prote
449	53.5	11.6	1138	2	T50454	hypothetical prote	522	53	11.4	1505	2	T00327	hypothetical prote
450	53.5	11.6	1358	2	B86241	hypothetical prote	523	53	11.4	1505	2	T00327	hypothetical prote
451	53.5	11.6	1444	1	A30588	140K adhesin precu	524	53	11.4	1505	2	T00327	hypothetical prote
452	53.5	11.6	1477	2	B43855	high-molecular-wei	525	53	11.4	1505	2	T00327	hypothetical prote
453	53.5	11.6	1502	1	RGBYH1	CYC1/CYP3 transcri	526	53	11.4	1505	2	T00327	hypothetical prote
454	53.5	11.6	1670	2	S71551	DNA-directed DNA p	527	53	11.4	1505	2	T00327	hypothetical prote
455	53.5	11.6	1808	2	T15099	hypothetical prote	528	53	11.4	1505	2	T00327	hypothetical prote
456	53.5	11.6	1986	2	S28353	probable polyketid	529	53	11.4	1505	2	T00327	hypothetical prote
457	53	11.5	68	2	JQ2005	hypothetical 7.5K	530	53	11.4	1505	2	T00327	hypothetical prote
458	53	11.5	72	2	T28324	ORF MSV163 hypothe	531	53	11.4	1505	2	T00327	hypothetical prote
459	53	11.5	173	2	A86400	protein F17L21.28	532	53	11.4	1505	2	T00327	hypothetical prote
460	53	11.5	233	2	C82360	cell division Alp-	533	53	11.4	1505	2	T00327	hypothetical prote
461	53	11.5	233	2	F70668	probable lipoprote	534	53	11.4	1505	2	T00327	hypothetical prote
462	53	11.5	238	2	T29250	hypothetical prote	535	53	11.4	1505	2	T00327	hypothetical prote
463	53	11.5	256	2	S64390	probable membrane	536	53	11.4	1505	2	T00327	hypothetical prote
464	53	11.5	271	2	D82314	transcription regu	537	53	11.4	1505	2	T00327	hypothetical prote
465	53	11.5	283	2	T04676	hypothetical prote	538	53	11.4	1505	2	T00327	hypothetical prote
466	53	11.5	285	1	E64461	fumarate hydratase	539	53	11.4	1505	2	T00327	hypothetical prote
467	53	11.5	328	2	G84826	hypothetical prote	540	53	11.4	1505	2	T00327	hypothetical prote

541 52.5 11.4 419 2 S17188 creatine kinase (E
542 52.5 11.4 423 2 B88450 protein F21H11.3 [
543 52.5 11.4 427 2 E96716 probable RNA-bind
544 52.5 11.4 439 2 B86168 hypothetical prote
545 52.5 11.4 447 2 S76218 3-phosphoshikimate
546 52.5 11.4 463 2 S63683 presenilin 1-463 -
547 52.5 11.4 466 2 A95355 probable inner-mem
548 52.5 11.4 467 2 S83936 presenilin 1, spli
549 52.5 11.4 476 2 H71936 proteinase DO - He
550 52.5 11.4 493 2 AG2738 glutamyl-trna amid
551 52.5 11.4 522 2 JC1204 vga protein - Stap
552 52.5 11.4 547 2 H85659 partial probable a
553 52.5 11.4 547 2 C90842 partial probable a
554 52.5 11.4 561 2 T34083 hypothetical prote
555 52.5 11.4 562 2 D84551 hypothetical protei
556 52.5 11.4 565 2 T38941 RNA binding protei
557 52.5 11.4 585 2 S43718 malate dehydrogena
558 52.5 11.4 590 1 S55035 myb-related protei
559 52.5 11.4 650 2 JC7937 transcription acti
560 52.5 11.4 651 2 T40789 acc operon express
561 52.5 11.4 656 2 T01573 earl protein - mai
562 52.5 11.4 728 2 S21913 BRcore-TN1-Q1-Z1
563 52.5 11.4 730 2 S64938 hypothetical prote
564 52.5 11.4 734 2 A22001 me12 protein - fis
565 52.5 11.4 750 1 COZPNE neurofilament trip
566 52.5 11.4 765 2 T49592 hypothetical prote
567 52.5 11.4 783 2 T38891 ribonucleoside-dip
568 52.5 11.4 788 1 S28302 S-receptor kinase
569 52.5 11.4 857 1 A41369 S-receptor kinase
570 52.5 11.4 858 1 J01677 hypothetical prote
571 52.5 11.4 859 2 T46372 structural protein
572 52.5 11.4 885 1 VCPVR2 testicular zinc fi
573 52.5 11.4 942 2 JC7316 centromere protein
574 52.5 11.4 943 2 A42681 probable membrane
575 52.5 11.4 955 2 G64866 hypothetical prote
576 52.5 11.4 1008 2 C84679 transcription acti
577 52.5 11.4 1008 2 S19033 protein W09G3.1a [
578 52.5 11.4 1015 2 B87992 probable secreted
579 52.5 11.4 1041 2 B81281 conserved hypothet
580 52.5 11.4 1052 2 AF2959 hypothetical prote
581 52.5 11.4 1090 2 H86806 hypothetical prote
582 52.5 11.4 1097 2 T45622 nitric-oxide synth
583 52.5 11.4 1206 2 T30555 protein phosphatas
584 52.5 11.4 1262 2 T30524 hypothetical prote
585 52.5 11.4 1341 2 H98323 DNA repair helicase
586 52.5 11.4 1493 2 A44224 hypothetical prote
587 52.5 11.4 1510 2 T33100 hypothetical prote
588 52.5 11.4 1626 2 T26318 hypothetical prote
589 52.5 11.4 1658 2 D75489 uncharacterized ph
590 52.5 11.4 1819 2 D97132 toucan gene protei
591 52.5 11.4 2176 2 T13806 genome polyprotein
592 52.5 11.4 2344 1 RRWRH genome polyprotein
593 52.5 11.4 2344 2 S55399 genome polyprotein
594 52.5 11.4 3016 2 S77300 hypothetical prote
595 52.5 11.4 4391 2 A38096 perlecan precursor
596 52 46 2 G89761 hypothetical prote
597 52 102 2 D71415 hypothetical prote
598 52 113 104 2 T13517 hypothetical prote
599 52 113 109 2 JW0100 azarene carbazole
600 52 113 123 2 A82813 hypothetical prote
601 52 113 136 1 LWBOA H+-transporting tw
602 52 113 139 2 A72471 hypothetical prote
603 52 113 147 2 F69124 hypothetical prote
604 52 113 148 2 S51276 hypothetical prote
605 52 113 163 2 C84510 En/Spm-like transp
606 52 113 172 2 S43462 mannose-binding le
607 52 113 173 2 A71872 hypothetical prote
608 52 113 182 2 E97246 hypothetical prote
609 52 113 185 2 AG3341 hypothetical prote
610 52 113 190 1 A44594 endo-1,4-beta-xyla
611 52 113 190 1 A44595 endo-1,4-beta-xyla
612 52 113 194 2 D70145 lipoprotein LA7 -
613 52 113 199 2 H73401 hypothetical prote

614 209 11.3 140273 outer surface prot
615 212 11.3 A88274 hypothetical prote
616 212 11.3 A86115 hypothetical prote
617 214 2 S06455 avenin precursor (
618 217 2 C70629 probable muc73 pro
619 222 2 S39154 xylanase 1 - fungu
620 223 2 S39883 endo-1,4-beta-xyla
621 231 2 D90943 hypothetical prote
622 231 2 H85791 hypothetical prote
623 231 2 H96837 unknown protein T2
624 256 2 H96837 hypothetical prote
625 262 2 C91055 protein GP80 [impo
626 273 2 T44657 probable oxidoredu
627 277 2 F85899 hypothetical prote
628 277 2 S50375 hypothetical prote
629 307 2 A72632 hypothetical prote
630 312 2 D72451 hydrogenase-2 smal
631 328 2 AE0885 hypothetical prote
632 334 2 G86865 hypothetical prote
633 342 2 A86364 hypothetical prote
634 343 2 T05221 hypothetical prote
635 349 2 T03736 nitrilase (EC 3.5.
636 351 1 MMECPB outer membrane por
637 351 2 D90662 outer membrane por
638 351 2 B85513 phospholipase Al p
639 363 2 T40797 60s ribosomal prot
640 363 2 G02786 uroporphyrinogen d
641 367 2 A24411 uroporphyrinogen d
642 369 2 S32793 biglycan precursor
643 371 1 E64821 Y111 protein precu
644 371 2 E90743 probable dehydroge
645 371 2 A85594 probable dehydroge
646 383 1 ALRZOC alpha-amylase (EC
647 392 2 A56123 streptogrisin D (E
648 392 2 T24666 hypothetical prote
649 394 2 G84016 arylalkylphospha
650 395 2 G90565 restriction modifi
651 395 2 AB2779 ABC transporter, m
652 410 2 AD2943 proline dipeptidas
653 410 2 F98339 hypothetical prote
654 412 2 S17758 tubulin beta chain
655 415 2 F97558 hypothetical prote
656 423 2 S11974 polyketide beta-ke
657 431 2 JC4692 C2 toxin component
658 438 1 S70602 cellulose 1,4-beta
659 442 2 F82486 C4-dicarboxylate t
660 444 2 JC1141 metacrylic-form-sp
661 453 2 B89942 hypothetical prote
662 460 2 F71292 probable GTP-bind
663 468 2 S75389 probable phenylala
664 482 2 T02355 hypothetical prote
665 498 1 VHVIV4 nucleoprotein - in
666 512 2 A87270 hypothetical prote
667 512 2 G96753 similar to disease
668 512 2 E27793 methyl coenzyme M
669 512 2 S03261 methl coenzyme M
670 512 2 T29897 hypothetical prote
671 512 2 C71460 hypothetical prote
672 512 2 A10042 thiol/disulfide in
673 512 2 F83471 asparaginase relat
674 601 2 T49437 fiber protein - mo
675 601 2 ERADFM threonyl-tRNA synt
676 613 1 A82479 hypothetical prote
677 613 2 T50281 hypothetical prote
678 658 2 F71410 hypoxia inducible
679 667 2 JC7771 probable lysophosp
680 673 2 T50281 structural protein
681 681 2 S3316 hypothetical prote
682 681 2 A83006 competence protein
683 746 2 A97979 82.3K alpha trans-
684 747 1 TNBEA2 hypothetical prote
685 829 2 T29372 epidermal growth f
686 843 2 A27131

687	52	11.3	908	2	T07409	lipoxigenase (EC 1	760	51.5	11.1	548	2	T40598	hypothetical prote
688	52	11.3	914	2	T25220	hypothetical prote	761	51.5	11.1	551	2	T50663	RCC1-like G exchan
689	52	11.3	1016	2	J00498	genome polypeptid	762	51.5	11.1	557	2	D96854	hemagglutinin prec
690	52	11.3	1023	2	AE1280	ATP-dependent dsDN	763	51.5	11.1	566	1	HMIVSA	transforming growt
691	52	11.3	1106	2	T19348	hypothetical prote	764	51.5	11.1	567	2	A44225	probable glycerone
692	52	11.3	1156	2	T23748	hypothetical prote	765	51.5	11.1	572	2	C96024	hypothetical prote
693	52	11.3	1206	2	T34021	protein kinase SK2	766	51.5	11.1	581	2	A71661	alkylglycerone-pho
694	52	11.3	1225	2	T09395	envelope polypept	767	51.5	11.1	611	2	JE0365	hypothetical prote
695	52	11.3	1231	2	T18532	serine/threonine pr	768	51.5	11.1	634	2	T00054	hypothetical prote
696	52	11.3	1484	2	T29275	hypothetical prote	769	51.5	11.1	640	2	G72339	threonine-tRNA lig
697	52	11.3	1489	2	T38842	probable RAS GTPas	770	51.5	11.1	663	2	D96549	protein hypothetic
698	52	11.3	1637	2	T00070	hypothetical prote	771	51.5	11.1	679	2	AD0507	probable glycosyl
699	52	11.3	1791	2	T24089	hypothetical prote	772	51.5	11.1	687	2	B87318	hypothetical prote
700	52	11.3	1849	2	C41859	IGA-specific metal	773	51.5	11.1	698	2	A90528	hypothetical prote
701	52	11.3	2004	2	F95133	immunoglobulin Al	774	51.5	11.1	708	2	A95214	cell wall surface
702	52	11.3	2140	2	F95074	serine proteinase,	775	51.5	11.1	719	2	B98078	hypothetical prote
703	52	11.3	2142	2	A97942	metalloproteinase	776	51.5	11.1	763	2	T18280	hypothetical prote
704	52	11.3	2211	1	KFB05	coagulation factor	777	51.5	11.1	823	2	F64526	adenine/cytosine D
705	52	11.3	2336	2	A45386	omega-conotoxin-se	778	51.5	11.1	823	2	T02812	probable membrane
706	52	11.3	3071	2	T45584	hypothetical prote	779	51.5	11.1	825	2	T27852	hypothetical prote
707	51.5	11.1	80	2	A54059	protein kinase C (780	51.5	11.1	828	2	C96639	protein R1F9.14 [1
708	51.5	11.1	101	2	AC1379	B. subtilis YfH1 p	781	51.5	11.1	835	2	F70363	cation transporter
709	51.5	11.1	112	1	SQRTSV	seminal vesicle se	782	51.5	11.1	862	1	QRMSLD	LDL receptor precu
710	51.5	11.1	112	1	I58340	androgen-dependent	783	51.5	11.1	872	2	S73948	Mg2+-transporting
711	51.5	11.1	120	2	S24698	Ig heavy chain V6	784	51.5	11.1	878	2	S56542	outer membrane ush
712	51.5	11.1	143	2	T29840	hypothetical prote	785	51.5	11.1	878	2	D91288	hypothetical prote
713	51.5	11.1	172	2	T27882	peptidylprolyl iso	786	51.5	11.1	878	2	G86129	hypothetical prote
714	51.5	11.1	203	2	A82917	ribosomal protein	787	51.5	11.1	887	2	T20941	hypothetical prote
715	51.5	11.1	208	2	C69869	spore cortex-lytic	788	51.5	11.1	921	2	AE1327	hypothetical prote
716	51.5	11.1	213	2	G84043	hypothetical prote	789	51.5	11.1	921	2	AE1698	isoleucyl-tRNA syn
717	51.5	11.1	217	1	STHUV2	somatotropin 2 pre	790	51.5	11.1	995	2	T50267	probable family 31
718	51.5	11.1	227	2	D81259	membrane antigen g	791	51.5	11.1	1035	2	T16588	hypothetical prote
719	51.5	11.1	234	1	Q0BE43	opacity protein op	792	51.5	11.1	1065	2	E67995	acriflavin resista
720	51.5	11.1	238	2	S36349	somatotropin 2 pre	793	51.5	11.1	1086	2	T17628	endo-1,4-beta-xyla
721	51.5	11.1	256	1	STHUV2	glutamine-binding	794	51.5	11.1	1125	2	T39052	hypothetical serin
722	51.5	11.1	262	2	B42478	peptidyl-prolyl ci	795	51.5	11.1	1166	2	S37692	probable tumor sup
723	51.5	11.1	267	2	G97956	triacylglycerol li	796	51.5	11.1	1180	2	E86719	hypothetical prote
724	51.5	11.1	268	2	S36694	hypothetical prote	797	51.5	11.1	1206	1	VGUVUV	M polyprotein - Ri
725	51.5	11.1	282	2	S46722	probable formate t	798	51.5	11.1	1217	2	T21403	hypothetical prote
726	51.5	11.1	284	2	G64052	hypothetical prote	799	51.5	11.1	1217	2	S15053	hypothetical prote
727	51.5	11.1	302	2	A84062	hypothetical prote	800	51.5	11.1	1245	2	D86260	protein T12C24.22
728	51.5	11.1	306	2	A75316	glucan endo-1,3-be	801	51.5	11.1	1377	2	D90538	hypothetical prote
729	51.5	11.1	330	2	B64140	hypothetical prote	802	51.5	11.1	1445	1	A48148	protein-tyrosine-p
730	51.5	11.1	331	2	T02343	[alpha] subunit of	803	51.5	11.1	1557	2	G86419	probable reverse t
731	51.5	11.1	337	2	AG1920	hypothetical prote	804	51.5	11.1	1966	2	T32552	hypothetical prote
732	51.5	11.1	347	2	H87153	hypothetical prote	805	51.5	11.1	2437	2	S53611	MBP1 protein - ra
733	51.5	11.1	356	2	S61061	hypothetical prote	806	51.5	11.1	2471	2	A9128	cell-fate determin
734	51.5	11.1	364	2	G82595	ABC transporter ph	807	51.5	11.1	2848	2	T32550	hypothetical prote
735	51.5	11.1	367	2	T28892	hypothetical prote	808	51.5	11.1	3436	2	S55659	tegument protein 6
736	51.5	11.1	374	2	JC1314	pectate lyase (EC	809	51.5	11.1	3591	1	S21010	filamentous hemagg
737	51.5	11.1	376	2	AG1420	hypothetical membr	810	51.5	11.1	4688	2	F82885	hypothetical prote
738	51.5	11.1	377	2	T26965	aminopeptidase - D	811	51	11.0	99	2	AD2270	hypothetical prote
739	51.5	11.1	380	2	A75500	probable integral	812	51	11.0	106	2	AE2124	hypothetical prote
740	51.5	11.1	385	2	E84449	phosphoprotein - N	813	51	11.0	128	1	MBRTS	hypothetical prote
741	51.5	11.1	395	2	S22827	NADH2 dehydrogenas	814	51	11.0	131	2	B91067	myelin basic prote
742	51.5	11.1	396	2	AE3396	succinyl-diaminopi	815	51	11.0	161	2	T23912	hypothetical lipop
743	51.5	11.1	403	2	H69362	glucose dehydrogen	816	51	11.0	163	2	G89983	hypothetical prote
744	51.5	11.1	412	1	S74981	hypothetical prote	817	51	11.0	171	1	MBPGB	STAPHYLOKINASE PRE
745	51.5	11.1	424	2	T67683	homeobox protein L	818	51	11.0	178	2	G96667	myelin basic prote
746	51.5	11.1	426	2	T04318	dihydroorotase (EC	819	51	11.0	181	2	AE2305	unknown protein, 5
747	51.5	11.1	428	1	DEBSO	hypothetical prote	820	51	11.0	193	2	H71881	hypothetical prote
748	51.5	11.1	437	2	AE2996	xylose transport p	821	51	11.0	193	2	H81874	probable outer mem
749	51.5	11.1	458	2	D98287	carboxy-terminal p	822	51	11.0	194	1	VOEC7P	fibrial protein 9
750	51.5	11.1	464	2	T10500	hypothetical prote	823	51	11.0	197	2	C89862	hypothetical prote
751	51.5	11.1	466	2	A82605	conjugal transfer	824	51	11.0	204	2	G97315	protein chain rele
752	51.5	11.1	484	2	T16695	hypothetical prote	825	51	11.0	215	2	F90655	hypothetical prote
753	51.5	11.1	490	2	D28951	S-mephenytoin 4-hy	826	51	11.0	217	1	R31V3	probable membrane
754	51.5	11.1	490	2	B38462	acetylglutamate sy	827	51	11.0	234	2	S53480	hypothetical prote
755	51.5	11.1	500	2	T40666	nicotinic acetylch	828	51	11.0	236	1	G83111	hypothetical prote
756	51.5	11.1	511	2	T43634	regulatory protein	829	51	11.0	243	2	A46472	cell surface prote
757	51.5	11.1	515	2	A25048	hypothetical prote	830	51	11.0	262	2	F98051	transcription plei
758	51.5	11.1	534	2	T25720	periplasmic trehal	831	51	11.0	269	2	G69597	phosphatidate cyti
759	51.5	11.1	545	2	H83342		832	51	11.0	270	2	AE1497	phosphoglycerate m

833	51	11.0	274	2	S10641	endA protein - Str	906	51	11.0	914	2	T07065	probable lipoxigen
834	51	11.0	274	2	F55229	DNA-entry nuclease	907	51	11.0	915	2	S54485	CES1 protein - yea
835	51	11.0	274	2	A99094	deoxyribonuclease	908	51	11.0	926	2	G96563	probable coatomer
836	51	11.0	275	2	E91285	probable integrase	909	51	11.0	926	2	T04679	hypothetical prote
837	51	11.0	276	2	F95259	conserved hypoteth	910	51	11.0	930	2	D71617	SERA antigen/papai
838	51	11.0	276	2	A99525	conserved hypoteth	911	51	11.0	942	2	T37539	probable guanine n
839	51	11.0	281	2	A81894	hydrogenase expres	912	51	11.0	960	1	A39651	discs-large tumor
840	51	11.0	281	2	D88637	protein W09G12.1 [913	51	11.0	995	2	A81398	formate dehydrogen
841	51	11.0	290	2	A82070	hypothetical prote	914	51	11.0	995	2	AE1773	formate dehydrogen
842	51	11.0	301	2	H86126	partial probable i	915	51	11.0	1009	2	C89910	hypothetical prote
843	51	11.0	309	2	B71195	hypothetical prote	916	51	11.0	1122	2	T00441	probable histidine
844	51	11.0	309	2	A73026	hypothetical prote	917	51	11.0	1219	2	T33509	hypothetical prote
845	51	11.0	317	2	H75453	electron transfer	918	51	11.0	1325	2	T13386	hypothetical prote
846	51	11.0	318	2	H98257	bifunctional carbo	919	51	11.0	1345	2	AB1775	hypothetical prote
847	51	11.0	319	2	AE0759	Cb1B protein limpo	920	51	11.0	1366	2	T00964	hypothetical prote
848	51	11.0	321	2	E81668	conserved hypoteth	921	51	11.0	1366	2	S76664	IgA-specific metal
849	51	11.0	323	2	E87298	hypothetical prote	922	51	11.0	1390	2	T14004	trfA protein - sli
850	51	11.0	327	1	XVHI1	site-specific DNA-	923	51	11.0	1430	2	S50596	hypothetical prote
851	51	11.0	328	1	MEMSB	goli-myeelin basic	924	51	11.0	1437	2	T31093	probable protein-t
852	51	11.0	330	2	T33944	hypothetical prote	925	51	11.0	1457	2	D81019	adhesion and penet
853	51	11.0	333	2	A82126	conserved hypoteth	926	51	11.0	1582	2	AC1153	adhesin homolog lm
854	51	11.0	339	2	T22607	hypothetical prote	927	51	11.0	1584	2	T18276	protein-tyrosine k
855	51	11.0	343	2	B86668	oligopeptide ABC t	928	51	11.0	1602	2	T31671	Rab3 GDP/GTP excha
856	51	11.0	344	2	D84450	hypothetical prote	929	51	11.0	1618	2	S21424	nestin - human
857	51	11.0	350	2	H87084	phenylalanyl-tRNA	930	51	11.0	1636	2	S60403	probable membrane
858	51	11.0	360	2	H86283	protein Tf15D22.8 [931	51	11.0	1671	2	S71628	sensory transducti
859	51	11.0	363	2	AE0616	outer membrane pro	932	51	11.0	1804	2	T34518	nestin - golden ha
860	51	11.0	372	2	H81291	hypothetical prote	933	51	11.0	1970	2	T03284	myoblast city prot
861	51	11.0	375	1	WZMCPB	pectate lyase (EC	934	51	11.0	2410	1	JQ1948	genome polyprotein
862	51	11.0	383	2	T21946	hypothetical prote	935	51	11.0	2626	2	T31099	myosin-RhoGAP prot
863	51	11.0	392	2	F84650	probable protein p	936	51	11.0	3507	2	T34513	hypothetical prote
864	51	11.0	395	2	F95179	aspartate aminotra	937	51	11.0	3623	2	T08618	intrinsic factor-B
865	51	11.0	395	2	F98046	hypothetical prote	938	51	11.0	4180	2	G83559	hypothetical prote
866	51	11.0	397	2	H72491	probable tyrosine	939	51	11.0	4836	2	T14346	hcr2 protein - mo
867	51	11.0	406	2	F87247	probable hydrolase	940	51	11.0	4936	2	AH2515	hypothetical prote
868	51	11.0	416	2	G83656	hypothetical prote	941	51	11.0	13288	2	T03099	mucin, submaxillar
869	51	11.0	419	2	G90213	hypothetical prote	942	50.5	10.9	67	2	F97389	50S ribosomal prot
870	51	11.0	422	2	S73369	hypothetical prote	943	50.5	10.9	74	2	AG2607	50S ribosomal prot
871	51	11.0	427	2	S83764	diaminobutyric aci	944	50.5	10.9	74	2	AE0950	hypothetical prote
872	51	11.0	428	2	S03767	cellulase (EC 3.2.	945	50.5	10.9	93	2	H64652	hypothetical prote
873	51	11.0	434	2	A75450	conserved hypoteth	946	50.5	10.9	125	2	B72517	hypothetical prote
874	51	11.0	437	2	G83996	stage IV sporulati	947	50.5	10.9	148	2	AD2365	hypothetical prote
875	51	11.0	448	1	F64105	biotin carboxylase	948	50.5	10.9	162	1	CSBY	peptidylprolyl iso
876	51	11.0	450	2	D97885	conserved hypoteth	949	50.5	10.9	162	2	D38257	glucan endo-1,3-be
877	51	11.0	476	2	C39481	serum response fac	950	50.5	10.9	163	1	PRSAK	staphylokinase - p
878	51	11.0	476	2	T17330	hypothetical prote	951	50.5	10.9	179	2	H46631	hypothetical prote
879	51	11.0	482	2	A57269	flagellin flaA - H	952	50.5	10.9	181	2	H64406	hypothetical prote
880	51	11.0	486	2	B39481	serum response fac	953	50.5	10.9	189	2	T28554	hypothetical prote
881	51	11.0	491	2	T12501	hypothetical prote	954	50.5	10.9	189	2	D36849	Al2L protein - var
882	51	11.0	499	2	G87410	hypothetical prote	955	50.5	10.9	189	2	B72165	Al3L protein - var
883	51	11.0	507	2	S25931	myocyte-specific e	956	50.5	10.9	190	2	S75797	hypothetical prote
884	51	11.0	544	2	D82526	ATP-dependent RNA	957	50.5	10.9	198	2	E71837	protein-export mem
885	51	11.0	559	2	F96500	hypothetical prote	958	50.5	10.9	201	2	G64676	protein translocat
886	51	11.0	568	2	JC7911	Na+-coupled citrat	959	50.5	10.9	205	1	NDECE8	colicin E8 (EC 3.1
887	51	11.0	586	2	S64779	probable membrane	960	50.5	10.9	205	1	PQ0032	colicin E9 (EC 3.1
888	51	11.0	608	2	T15979	hypothetical prote	961	50.5	10.9	233	2	T48725	hypothetical prote
889	51	11.0	609	2	T22803	hypothetical prote	962	50.5	10.9	244	1	I40172	hypothetical prote
890	51	11.0	625	2	S34035	hypothetical prote	963	50.5	10.9	261	2	D75335	hypothetical prote
891	51	11.0	642	2	S64348	hypothetical prote	964	50.5	10.9	262	2	T40941	hypothetical prote
892	51	11.0	661	2	S21221	hemocyanin chain c	965	50.5	10.9	269	2	C89918	hypothetical serin
893	51	11.0	670	2	T29898	kinesin protein OS	966	50.5	10.9	270	2	B75581	probable cytochrom
894	51	11.0	672	2	S54351	kinesin osm-3 - Ca	967	50.5	10.9	271	2	T37222	probable secreted
895	51	11.0	715	2	T12534	hypothetical prote	968	50.5	10.9	275	1	WMBEH4	UL34 protein - hum
896	51	11.0	717	2	T15340	hypothetical prote	969	50.5	10.9	277	2	D86205	protein F10K1.23 [
897	51	11.0	719	2	A30047	enhancer of split	970	50.5	10.9	289	2	F81399	succinate-CoA liga
898	51	11.0	735	2	T47594	hypothetical prote	971	50.5	10.9	307	2	B40711	RNA polymerase II
899	51	11.0	741	2	T40095	zinc finger, C3HC4	972	50.5	10.9	311	2	E81703	phospholipase D fa
900	51	11.0	746	2	C95110	competence protei	973	50.5	10.9	317	2	E82815	ribokinase XF0366
901	51	11.0	757	2	T02884	D-(-)-3-hydroxybut	974	50.5	10.9	328	2	T50104	hypothetical prote
902	51	11.0	822	2	S56823	probable membrane	975	50.5	10.9	331	2	AG0599	Hyd-family secret
903	51	11.0	836	2	S49940	cell division cont	976	50.5	10.9	337	2	G95922	probable glycosylt
904	51	11.0	841	2	S69563	suppressor protein	977	50.5	10.9	338	2	T24743	hypothetical prote
905	51	11.0	871	2	T43427	pobl protein - fis	978	50.5	10.9	342	2	S50400	hypothetical prote

979	50.5	10.9	343	2	155123	fimbrial lectin, N	1052	50.5	10.9	1083	2	559780	hypothetical prote
980	50.5	10.9	343	2	141205	adhesin - Escheric	1053	50.5	10.9	1107	2	AC0976	probable autotrans
981	50.5	10.9	344	2	A42359	fimbrial adhesin F	1054	50.5	10.9	1107	2	E84433	hypothetical prote
982	50.5	10.9	351	2	AH1331	hypothetical prote	1055	50.5	10.9	1134	2	C88040	protein F47Fe.5 [i
983	50.5	10.9	353	2	S15717	pectate lyase (EC	1056	50.5	10.9	1143	2	T10636	hypothetical prote
984	50.5	10.9	376	2	G70301	N-acetylornithine	1057	50.5	10.9	1242	2	F97877	phosphoribosylform
985	50.5	10.9	379	2	A48936	nitrite reductase	1058	50.5	10.9	1305	2	AB0168	probable cell divi
986	50.5	10.9	385	2	C75921	hypothetical prote	1059	50.5	10.9	1376	1	VCBEP6	major capsid prote
987	50.5	10.9	391	2	C69673	penicillin-binding	1060	50.5	10.9	1427	2	I51869	tumor suppressor -
988	50.5	10.9	397	2	T40539	zinc finger protei	1061	50.5	10.9	1433	2	G01946	nitric-oxide synth
989	50.5	10.9	404	2	D84533	hypothetical prote	1062	50.5	10.9	1433	2	S54587	CAR8 protein - yea
990	50.5	10.9	420	2	T14911	bZIP DNA-binding p	1063	50.5	10.9	1472	2	H82802	fimbrial assembly
991	50.5	10.9	429	2	D87375	lpsE protein [lipo	1064	50.5	10.9	1513	2	S45768	mitotic spindle p
992	50.5	10.9	437	2	B87327	sensor histidine k	1065	50.5	10.9	1574	1	A38454	myosin MYO2 - yea
993	50.5	10.9	447	2	T21716	hypothetical prote	1066	50.5	10.9	1588	2	A86036	probable adhesin Z
994	50.5	10.9	450	2	AB0484	glutathione-disulf	1067	50.5	10.9	1588	2	H91188	probable adhesin E
995	50.5	10.9	461	2	S34472	MFH-1 protein - mo	1068	50.5	10.9	1758	2	T30560	resistance protein
996	50.5	10.9	472	2	S53866	cytosine methylase	1069	50.5	10.9	1784	2	T02844	cdc16-related prot
997	50.5	10.9	474	2	S77247	hypothetical prote	1070	50.5	10.9	1870	2	D88486	protein F20H11.2 [
998	50.5	10.9	490	2	F38462	S-mephenytoin 4'-h	1071	50.5	10.9	2021	2	A97859	190-kDa cell surfa
999	50.5	10.9	492	2	B86253	hypothetical prote	1072	50.5	10.9	2067	2	A42854	probable spindle p
1000	50.5	10.9	495	2	T18835	hypothetical prote	1073	50.5	10.9	2180	2	A47851	zinc-finger protei
1001	50.5	10.9	499	2	D72342	tldD protein - The	1074	50.5	10.9	2271	2	F90073	hypothetical prote
1002	50.5	10.9	501	2	JC7877	toxin-60A - Okinaw	1075	50.5	10.9	2344	2	S64740	genome polyprotein
1003	50.5	10.9	503	2	S00336	legumin B LegJ pre	1076	50.5	10.9	2368	2	S46005	ESR1 protein - yea
1004	50.5	10.9	504	2	A11960	hypothetical prote	1077	50.5	10.9	2638	1	A42545	genome polyprotein
1005	50.5	10.9	512	2	S15691	hypothetical prote	1078	50.5	10.9	3169	2	T00296	toxin B - Escheric
1006	50.5	10.9	512	2	A53219	singed protein - f	1079	50.5	10.9	5188	2	B85347	probable RIX famil
1007	50.5	10.9	519	2	S13874	nicotinic acetylch	1080	50.5	10.9	5291	2	F90696	hypothetical prote
1008	50.5	10.9	538	2	A57624	retinoblastoma pro	1081	50	10.8	65	2	AI0612	hypothetical prote
1009	50.5	10.9	567	2	S76847	phosphoglucutase	1082	50	10.8	92	2	G69229	hypothetical prote
1010	50.5	10.9	567	2	G90537	lipoprotein [lipo	1083	50	10.8	93	2	A97190	hypothetical prote
1011	50.5	10.9	569	1	URKCBP	urease (EC 3.5.1.5	1084	50	10.8	111	2	S44787	D2007.1 protein -
1012	50.5	10.9	581	1	NDEC82	colicin E2 (EC 3.1	1085	50	10.8	113	2	E82019	probable periplasm
1013	50.5	10.9	583	2	T11624	spindle poison sen	1086	50	10.8	115	2	S09866	hypothetical prote
1014	50.5	10.9	586	2	B41627	furin (EC 3.4.21.7	1087	50	10.8	127	2	PC2270	cytochrome P450 pr
1015	50.5	10.9	603	2	A75373	probable N-acetyl	1088	50	10.8	127	2	F90696	cytochrome P450 pr
1016	50.5	10.9	627	2	AD1818	N-acetylneuramoyl-L	1089	50	10.8	136	1	S31769	H+-transporting tw
1017	50.5	10.9	644	2	B71409	hypothetical prote	1090	50	10.8	138	2	S18587	hypothetical prote
1018	50.5	10.9	651	2	A96591	NPK1-related prote	1091	50	10.8	151	1	GCCH	glucagon precursor
1019	50.5	10.9	658	2	D69431	methionine-tRNA l1	1092	50	10.8	154	2	AI0132	hypothetical prote
1020	50.5	10.9	670	2	T05495	hypothetical prote	1093	50	10.8	158	2	B82190	hypothetical prote
1021	50.5	10.9	688	2	AI2516	hypothetical prote	1094	50	10.8	163	2	S43762	mannose-binding le
1022	50.5	10.9	691	1	A36295	heat shock transcr	1095	50	10.8	167	2	A37246	myelin basic prote
1023	50.5	10.9	694	2	S32958	probable membrane	1096	50	10.8	172	2	AH1291	hypothetical prote
1024	50.5	10.9	707	2	AI3290	transketolase (EC	1097	50	10.8	175	2	A71680	cytochrome C (cyto
1025	50.5	10.9	707	2	A35804	nucleolin - human	1098	50	10.8	188	2	B84728	probable alanine a
1026	50.5	10.9	712	2	T48361	hypothetical prote	1099	50	10.8	190	2	D75319	3-methyladenine gl
1027	50.5	10.9	712	2	S64828	SSK1 protein - yea	1100	50	10.8	206	2	I51301	proglucagon - chic
1028	50.5	10.9	725	2	T43092	probable transfer	1101	50	10.8	209	2	T12075	ribonuclease (EC 3
1029	50.5	10.9	725	2	F82634	tail-specific prot	1102	50	10.8	213	1	C44056	22K protein - cani
1030	50.5	10.9	737	2	S62561	ATP dependent RNA	1103	50	10.8	218	2	AH1837	hypothetical prote
1031	50.5	10.9	754	2	AF0118	probable kinase YP	1104	50	10.8	236	1	A35649	cell surface prote
1032	50.5	10.9	775	2	T07172	subtilisin-like pr	1105	50	10.8	236	2	S57986	NBP2 protein - yea
1033	50.5	10.9	783	2	A41627	furin (EC 3.4.21.7	1106	50	10.8	240	2	AG2529	transcription regu
1034	50.5	10.9	784	2	T45027	hypothetical prote	1107	50	10.8	247	2	T08032	chalcone isomerase
1035	50.5	10.9	799	2	PC4106	chitinase (EC 3.2.	1108	50	10.8	266	2	S60674	hypothetical prote
1036	50.5	10.9	800	2	C89911	topoisomerase IV s	1109	50	10.8	267	2	D95089	hypothetical prote
1037	50.5	10.9	800	2	S54427	gyrase-like protei	1110	50	10.8	269	2	T32639	hypothetical prote
1038	50.5	10.9	820	2	A40633	chitinase (EC 3.2.	1111	50	10.8	275	2	C84673	hypothetical prote
1039	50.5	10.9	822	2	T09221	exocyst complex pr	1112	50	10.8	277	2	F84336	hypothetical prote
1040	50.5	10.9	838	2	G64556	flagellin B homolo	1113	50	10.8	284	2	T04674	hypothetical prote
1041	50.5	10.9	841	2	T20221	hypothetical prote	1114	50	10.8	287	2	T41694	hypothetical prote
1042	50.5	10.9	918	2	I58178	glutamate receptor	1115	50	10.8	288	2	D97113	probable GTPase (Y
1043	50.5	10.9	928	2	C81265	probable lipoprote	1116	50	10.8	295	2	D83195	probable transcrip
1044	50.5	10.9	937	2	S78561	CS3 pilin syntheti	1117	50	10.8	296	2	T47598	hypothetical prote
1045	50.5	10.9	946	2	D96503	protein F9C16.9 [i	1118	50	10.8	300	2	AE3255	3-oxoacyl-(acyl-ca
1046	50.5	10.9	946	2	A96748	hypothetical prote	1119	50	10.8	310	2	T01939	hypothetical prote
1047	50.5	10.9	978	2	D81411	probable lipoprote	1120	50	10.8	314	2	A84960	probable signal pe
1048	50.5	10.9	1036	2	S55984	probable membrane	1121	50	10.8	319	2	T01546	hypothetical prote
1049	50.5	10.9	1041	2	T31437	integrin alpha cha	1122	50	10.8	324	2	T52609	cysteine synthase
1050	50.5	10.9	1061	2	S75508	acriflavin resista	1123	50	10.8	325	1	TVHUA5	transforming prote
1051	50.5	10.9	1075	2	T34223	hypothetical prote	1124	50	10.8	326	2	S67249	probable membrane

1125	50	10.8	335	2	AD1314	peptidase homolog	1198	50	10.8	709	2	T39930	probable atp-depen
1126	50	10.8	337	2	S31131	hypothetical prote	1199	50	10.8	714	2	S46811	hypothetical prote
1127	50	10.8	340	2	F88545	protein F59B2.11 {	1200	50	10.8	719	2	S55119	hypothetical prote
1128	50	10.8	347	2	S10571	mucin 1 precursor,	1201	50	10.8	736	2	JC7518	subtilisin-like se
1129	50	10.8	348	2	T72627	hypothetical prote	1202	50	10.8	744	2	A97939	single-stranded DN
1130	50	10.8	350	2	T76509	hypothetical prote	1203	50	10.8	756	2	JC5886	signaling mediator
1131	50	10.8	360	2	S74691	iron transport pro	1204	50	10.8	764	2	T45793	hypothetical prote
1132	50	10.8	363	2	E89912	prephenate dehydro	1205	50	10.8	788	2	S53397	actin-interacting
1133	50	10.8	375	2	S26059	probable transform	1206	50	10.8	790	2	E85726	hypothetical prote
1134	50	10.8	376	2	S45763	hypothetical prote	1207	50	10.8	790	2	D90851	hypothetical prote
1135	50	10.8	380	2	H95129	glucose-1-phosphat	1208	50	10.8	792	2	B64903	ydbB protein precu
1136	50	10.8	391	2	H90968	probable host spec	1209	50	10.8	804	2	H75549	glycogen debranchi
1137	50	10.8	391	2	H90996	probable host spec	1210	50	10.8	809	1	S43217	ubiquitin-protein
1138	50	10.8	392	2	H81408	probable periplasm	1211	50	10.8	834	2	S74654	sensory transducti
1139	50	10.8	392	2	B69821	conserved hypothet	1212	50	10.8	834	2	A00279	probable heat shoc
1140	50	10.8	392	2	C84905	probable extensin	1213	50	10.8	846	2	T28055	probable virulence
1141	50	10.8	397	2	S64841	hypothetical prote	1214	50	10.8	848	2	JC2482	hypothetical prote
1142	50	10.8	400	2	C75336	serine proteinase,	1215	50	10.8	856	1	JC2482	S-receptor kinase
1143	50	10.8	409	2	T20847	hypothetical prote	1216	50	10.8	868	2	B89897	conserved hypothet
1144	50	10.8	410	2	AG1288	aminopeptidases ho	1217	50	10.8	913	2	B8487	hypothetical prote
1145	50	10.8	410	2	AF1660	aminopeptidases ho	1218	50	10.8	972	2	B36640	isoleucine-tRNA li
1146	50	10.8	413	1	S03631	homeotic protein S	1219	50	10.8	972	2	T16094	hypothetical prote
1147	50	10.8	417	2	JQ2142	chaperone ANU1 pro	1220	50	10.8	982	1	VCLJVS	env polyprotein pr
1148	50	10.8	425	2	S68305	gag polyprotein -	1221	50	10.8	983	1	E45390	env polyprotein pr
1149	50	10.8	429	2	T17920	hypothetical prote	1222	50	10.8	986	2	AH3056	sarcosine oxidase
1150	50	10.8	431	2	S46594	probable transcrip	1223	50	10.8	986	2	F98229	sarcosine oxidase
1151	50	10.8	433	2	D87408	ATPase, AAA family	1224	50	10.8	1015	2	T32984	hypothetical prote
1152	50	10.8	433	2	T48118	hypothetical prote	1225	50	10.8	1022	2	T49683	probable oxoglutar
1153	50	10.8	444	2	H41396	probable secreted	1226	50	10.8	1023	2	A51643	ATP-dependent dsDN
1154	50	10.8	445	2	T48325	hypothetical prote	1227	50	10.8	1047	2	A59246	HIRA protein - fru
1155	50	10.8	450	2	T51075	hypothetical prote	1228	50	10.8	1070	1	RNNTB	DNA-directed RNA p
1156	50	10.8	452	2	T00840	probable senescenc	1229	50	10.8	1076	1	A35622	nuclear pore prote
1157	50	10.8	457	2	B85020	probable NAM-like	1230	50	10.8	1090	2	T30576	glucan synthase -
1158	50	10.8	463	2	T14884	hypothetical prote	1231	50	10.8	1094	2	A53435	vesicular transpor
1159	50	10.8	465	2	D82804	GTP-binding protei	1232	50	10.8	1097	2	F96538	hypothetical prote
1160	50	10.8	468	2	C96818	hypothetical prote	1233	50	10.8	1162	2	E84431	probable Na+/H+ an
1161	50	10.8	469	2	JC4523	apoptosis protein	1234	50	10.8	1254	2	G86379	protein F5A9.24 li
1162	50	10.8	472	2	T04699	hypothetical prote	1235	50	10.8	1303	1	S27396	phytochrome / prot
1163	50	10.8	473	2	S36241	penicillin-binding	1236	50	10.8	1318	2	T39066	hypothetical prote
1164	50	10.8	473	2	S36239	penicillin-binding	1237	50	10.8	1350	2	T42697	hypothetical prote
1165	50	10.8	473	2	T46305	hypothetical prote	1238	50	10.8	1484	2	T42632	breast cancer tumo
1166	50	10.8	476	2	T40086	hypothetical prote	1239	50	10.8	1594	2	T43072	hemolysin A - Edwa
1167	50	10.8	483	2	AB0458	Trk system potassi	1240	50	10.8	1672	2	C81675	polymorphic membra
1168	50	10.8	488	2	G69439	flavoprotein (fprA	1241	50	10.8	1799	2	AD1895	serine/threonine k
1169	50	10.8	489	2	D87551	glutamyI-tRNA (Gln)	1242	50	10.8	1885	2	JQ2183	hypothetical prote
1170	50	10.8	491	2	T21421	hypothetical prote	1243	50	10.8	2244	2	F90563	hypothetical prote
1171	50	10.8	492	2	F96985	probable alttronate	1244	50	10.8	2261	1	A42548	genome polyprotein
1172	50	10.8	500	2	S44760	C14B9.3 protein -	1245	50	10.8	2548	2	E59435	myosin IXA import
1173	50	10.8	514	2	D84584	probable protein p	1246	50	10.8	2560	1	I40457	peptide synthetase
1174	50	10.8	554	2	S59235	hypothetical prote	1247	50	10.8	3442	2	B82589	hemagglutinin-like
1175	50	10.8	555	2	AD0166	conserved hypothet	1248	50	10.8	3455	2	B82519	hypothetical prote
1176	50	10.8	557	2	I50429	transforming growt	1249	50	10.8	5005	2	F82884	conserved hypothet
1177	50	10.8	561	2	H86442	unknown protein (i	1250	49.5	10.7	90	1	D69782	conserved hypothet
1178	50	10.8	570	2	S38798	hexose transport p	1251	49.5	10.7	97	2	A70230	lilS19-1 protein -
1179	50	10.8	573	2	A41319	3-oxosteroid 1-deh	1252	49.5	10.7	119	2	F45348	hypothetical prote
1180	50	10.8	575	1	RD8YC	1-pyrroline-5-carb	1253	49.5	10.7	120	2	H75532	conserved hypothet
1181	50	10.8	577	2	D44307	phosphoprotein pho	1254	49.5	10.7	122	2	AG0221	hypothetical prote
1182	50	10.8	585	1	SXAD32	peripentonal hexon	1255	49.5	10.7	126	2	A82826	hypothetical prote
1183	50	10.8	585	1	SXADH5	peripentonal hexon	1256	49.5	10.7	126	2	T29997	hypothetical prote
1184	50	10.8	589	2	T49653	related to sly41 p	1257	49.5	10.7	143	2	E71129	hypothetical prote
1185	50	10.8	592	2	A42100	transforming growt	1258	49.5	10.7	158	2	E82818	conserved hypothet
1186	50	10.8	594	2	D95286	hypothetical prote	1259	49.5	10.7	163	2	F97332	hypothetical prote
1187	50	10.8	605	1	A48665	methionyl-CoA	1260	49.5	10.7	165	2	G30338	comG operon protei
1188	50	10.8	614	1	S10032	urease (EC 3.5.1.5	1261	49.5	10.7	171	2	T27371	peptidylprolyl iso
1189	50	10.8	614	2	A96716	probable fructokin	1262	49.5	10.7	177	2	S43647	von Ebner's gland
1190	50	10.8	616	2	G86890	proline-tRNA ligas	1263	49.5	10.7	195	2	A96779	myelin basic prote
1191	50	10.8	642	2	D88951	protein C38C3.7 (i	1264	49.5	10.7	197	1	MBHUB	protein F2D10.20 l
1192	50	10.8	649	2	T40863	glycerol-3-phospha	1265	49.5	10.7	197	2	G86339	minor outer capsid
1193	50	10.8	670	2	JC5887	signaling mediator	1266	49.5	10.7	198	1	MXRVM	probable luxR-fami
1194	50	10.8	681	2	T23454	hypothetical prote	1267	49.5	10.7	200	2	AF0359	cob(I) alamin adeno
1195	50	10.8	708	2	JC4364	gelatinase B (EC 3	1268	49.5	10.7	207	2	H75618	hypothetical prote
1196	50	10.8	708	2	JC2323	lactoferrin - goat	1269	49.5	10.7	215	2	T48010	hypothetical prote
1197	50	10.8	709	2	B95071	single-stranded-DN	1270	49.5	10.7	215	2	AB3315	extensin-like prot

1271	49.5	10.7	219	2	S62804	ribosomal protein	1344	49.5	10.7	579	2	AE2774	conserved hypother
1272	49.5	10.7	222	2	D69014	conserved hypother	1345	49.5	10.7	592	2	F81417	MCP-domain signal
1273	49.5	10.7	228	2	A98337	hypothetical prote	1346	49.5	10.7	617	2	JC4559	methylmalonyl-CoA
1274	49.5	10.7	228	2	AE2956	haloacid dehalogen	1347	49.5	10.7	630	2	C98351	oligopeptide-bind
1275	49.5	10.7	233	2	S36350	opacity protein op	1348	49.5	10.7	632	2	T00679	hypothetical prote
1276	49.5	10.7	245	2	C29835	TraP protein - Es	1349	49.5	10.7	671	2	AE0486	probable membrane
1277	49.5	10.7	250	2	S29240	proteasome endopep	1350	49.5	10.7	698	1	IKEC5B	colicin V secretio
1278	49.5	10.7	253	2	S73793	probable lipoprote	1351	49.5	10.7	704	2	T39202	heat shock protein
1279	49.5	10.7	264	2	A31818	merozoite 45K sur	1352	49.5	10.7	707	1	S69781	outer membrane pro
1280	49.5	10.7	265	2	AE0256	phage regulatory p	1353	49.5	10.7	739	2	B86434	protein Fl78.27 [
1281	49.5	10.7	273	2	E64316	hypothetical prote	1354	49.5	10.7	769	2	B96613	hypothetical prote
1282	49.5	10.7	278	2	T19813	hypothetical prote	1355	49.5	10.7	777	2	C86454	hypothetical prote
1283	49.5	10.7	290	2	AF0096	prolipoprotein dia	1356	49.5	10.7	787	2	S54535	hypothetical prote
1284	49.5	10.7	293	2	A96946	N-dimethylarginine	1357	49.5	10.7	862	2	B36786	hypothetical prote
1285	49.5	10.7	296	2	A34543	speract precursor	1358	49.5	10.7	877	1	A25962	mitosis inhibitor
1286	49.5	10.7	300	2	A55792	beta-lactamase (EC	1359	49.5	10.7	879	1	QRR1LD	LDL receptor precu
1287	49.5	10.7	308	2	D72768	probable electron	1360	49.5	10.7	881	2	C87471	TonB-dependent rec
1288	49.5	10.7	313	2	A83951	riboflavin kinase	1361	49.5	10.7	884	2	S61569	hypothetical prote
1289	49.5	10.7	319	2	F98987	Alpha-Hemolysin pr	1362	49.5	10.7	888	2	S61619	STU2 protein - yea
1290	49.5	10.7	319	2	S69209	alpha-toxin precu	1363	49.5	10.7	900	2	S73748	alanine-tRNA ligas
1291	49.5	10.7	336	2	AG2686	ABC transporter, s	1364	49.5	10.7	916	2	S22864	DNA topoisomerase
1292	49.5	10.7	336	2	D97468	hypothetical prote	1365	49.5	10.7	939	2	H71532	valine-cRNA ligase
1293	49.5	10.7	340	2	T10950	starch phosphoryla	1366	49.5	10.7	944	2	T38130	probable helicase
1294	49.5	10.7	346	2	T51551	quinone oxidoreduc	1367	49.5	10.7	955	2	T10947	starch phosphoryla
1295	49.5	10.7	347	2	S44995	pectate lyase - Er	1368	49.5	10.7	968	2	T29532	hypothetical prote
1296	49.5	10.7	352	1	K1BE84	thymidine kinase (1369	49.5	10.7	986	2	T33135	hypothetical prote
1297	49.5	10.7	352	2	T42582	thymidine kinase (1370	49.5	10.7	992	2	T05335	hypothetical prote
1298	49.5	10.7	355	2	JE0385	NADH2 dehydrogenas	1371	49.5	10.7	1015	2	T13062	hypothetical prote
1299	49.5	10.7	357	2	A99272	inorganic phosphat	1372	49.5	10.7	1017	2	G85055	probable polyprote
1300	49.5	10.7	362	2	Ar2113	hypothetical prote	1373	49.5	10.7	1023	2	T13068	CLOCK protein - fr
1301	49.5	10.7	364	2	T16376	hypothetical prote	1374	49.5	10.7	1037	2	T13071	CLOCK protein - fr
1302	49.5	10.7	371	2	T16391	hypothetical prote	1375	49.5	10.7	1037	2	E81980	pilus-associated p
1303	49.5	10.7	375	2	T41661	probable alanine r	1376	49.5	10.7	1038	1	B42641	kinesin-related pr
1304	49.5	10.7	379	2	T19773	hypothetical prote	1377	49.5	10.7	1091	2	S57112	USN1 protein - yea
1305	49.5	10.7	380	2	T39015	probable DNA-J-lik	1378	49.5	10.7	1094	2	T50651	AP3-complex beta-3
1306	49.5	10.7	381	2	D70669	coenzyme F420-depe	1379	49.5	10.7	1152	2	T21853	hypothetical prote
1307	49.5	10.7	381	2	JC7650	pectin lyase (EC 4	1380	49.5	10.7	1152	2	AE1852	hypothetical prote
1308	49.5	10.7	382	2	B65575	hypothetical prote	1381	49.5	10.7	1173	2	T25893	hypothetical prote
1309	49.5	10.7	382	2	A72049	hypothetical prote	1382	49.5	10.7	1197	1	VGURF	W polyprotein - Ri
1310	49.5	10.7	383	2	F71550	probable endonucle	1383	49.5	10.7	1257	2	T00486	serine/threonine-s
1311	49.5	10.7	386	2	S36865	cathepsin B (EC 3.	1384	49.5	10.7	1290	2	JCS473	dextranucrase (EC
1312	49.5	10.7	396	2	S49592	cytochrome b-like	1385	49.5	10.7	1309	2	T39379	sexual differentia
1313	49.5	10.7	399	2	A55577	formaldehyde dehyd	1386	49.5	10.7	1430	2	AF0351	probable autotrans
1314	49.5	10.7	404	2	T48947	hypothetical prote	1387	49.5	10.7	1439	2	T02087	gag/pol polyprotei
1315	49.5	10.7	404	2	T46063	hypothetical prote	1388	49.5	10.7	1442	1	B48148	protein-tyrosine-p
1316	49.5	10.7	422	2	G89960	conserved hypother	1389	49.5	10.7	1577	2	A35140	hemolysin A precu
1317	49.5	10.7	423	2	B86214	hypothetical prote	1390	49.5	10.7	1599	2	S22737	glucosyltransferas
1318	49.5	10.7	445	2	T34352	hypothetical prote	1391	49.5	10.7	1644	2	AC0823	probable lipoprote
1319	49.5	10.7	445	2	T49318	probable SOf1 prot	1392	49.5	10.7	1702	2	A41859	IgA-specific metal
1320	49.5	10.7	446	2	A69750	erythromycin ester	1393	49.5	10.7	1720	2	T07258	cell division prot
1321	49.5	10.7	447	2	T20552	hypothetical prote	1394	49.5	10.7	2098	2	T18397	protein CTsp - mal
1322	49.5	10.7	449	2	S48173	variable surface g	1395	49.5	10.7	2325	2	T15566	hypothetical prote
1323	49.5	10.7	453	2	T01114	hypothetical prote	1396	49.5	10.7	2412	1	JQ1537	genome polyprotein
1324	49.5	10.7	459	2	AI1874	two-component sens	1397	49.5	10.7	2523	2	T18477	hypothetical prote
1325	49.5	10.7	463	2	F88991	protein K0B09.2 [i	1398	49.5	10.7	3562	2	A47171	chondroitin sulfat
1326	49.5	10.7	473	2	F83728	phosphoribosylpro	1399	49.5	10.7	4152	2	T31102	filamentous hemag
1327	49.5	10.7	476	2	T20982	hypothetical prote	1400	49.5	10.7	4377	2	A55575	ankyrin 3, long sp
1328	49.5	10.7	482	2	B87382	hypothetical prote	1401	49.5	10.7	4919	2	T31105	hypothetical prote
1329	49.5	10.7	482	1	C5SV	catalase (EC 1.11.	1402	49	10.6	81	2	C97386	hypothetical prote
1330	49.5	10.7	498	1	VH1VX5	nucleoprotein - in	1403	49	10.6	93	2	H64501	conserved hypother
1331	49.5	10.7	502	2	S69578	SPS2 protein - yea	1404	49	10.6	97	2	S01502	NADH2 dehydrogenas
1332	49.5	10.7	507	2	S64388	hypothetical prote	1405	49	10.6	109	2	C84974	protein-export mem
1333	49.5	10.7	510	2	S42090	Not(56) protein -	1406	49	10.6	113	2	F65188	hypothetical 12.1
1334	49.5	10.7	511	2	S10527	endoglucanase B pr	1407	49	10.6	125	2	S64890	probable membrane
1335	49.5	10.7	514	2	H97819	hypothetical prote	1408	49	10.6	136	2	D69653	transcription regu
1336	49.5	10.7	514	2	D71667	propionyl-CoA carb	1409	49	10.6	149	2	B40463	integrin alpha-6 c
1337	49.5	10.7	541	2	S51799	nucleoporin NUP57	1410	49	10.6	151	2	I46626	rearranged T-cell
1338	49.5	10.7	546	2	C97554	hypothetical prote	1411	49	10.6	163	2	S02330	staphylokinase - p
1339	49.5	10.7	559	2	G84132	methyl-accepting c	1412	49	10.6	171	2	D90372	hypothetical prote
1340	49.5	10.7	562	1	ERADN2	60.5K fiber protei	1413	49	10.6	177	2	S08161	hydrophobic molecu
1341	49.5	10.7	565	2	G64532	methyl-accepting c	1414	49	10.6	180	2	T32506	hypothetical prote
1342	49.5	10.7	573	2	C86266	F3F19.21 protein -	1415	49	10.6	184	2	E90335	hypothetical prote
1343	49.5	10.7	579	2	S51528	D-lactate dehydrog	1416	49	10.6	185	2	AD1026	hypothetical prote

1417 49 10.6 193 2 G69707 signal peptidase I
1418 49 10.6 199 2 A32183 tropomyosin TPM1 -
1419 49 10.6 199 2 H88987 protein C50H11.3 {
1420 49 10.6 200 2 H83059 hypothetical prote
1421 49 10.6 201 2 H71059 hypothetical prote
1422 49 10.6 202 2 A39139 hypothetical prote
1423 49 10.6 202 2 A33149 acetyltransferase
1424 49 10.6 204 2 G39965 hypothetical prote
1425 49 10.6 205 2 T38667 zinc finger protei
1426 49 10.6 206 2 T37552 conserved hypothe
1427 49 10.6 207 1 S31011 probable phospho
1428 49 10.6 211 2 I40282 outer surface prot
1429 49 10.6 213 2 S25647 ookinete surface p
1430 49 10.6 219 2 AF0639 flagellar basal bo
1431 49 10.6 220 1 ISFJCB chalcone isomerase
1432 49 10.6 261 2 B90298 hypothetical prote
1433 49 10.6 262 1 JQ1738 coat protein - sha
1434 49 10.6 264 2 F83952 phosphatidate cyti
1435 49 10.6 273 2 A99963 conserved hypothet
1436 49 10.6 276 2 C90002 phosphomethylpyrim
1437 49 10.6 278 2 D83474 hypothetical prote
1438 49 10.6 281 2 T24330 hypothetical prote
1439 49 10.6 281 2 F87442 signal peptidase I
1440 49 10.6 284 2 A92729 phosphatidate cyti
1441 49 10.6 285 2 T35195 probable serine pr
1442 49 10.6 294 2 AC2078 hypothetical prote
1443 49 10.6 298 2 H83163 probable transcrip
1444 49 10.6 298 2 F90495 conserved hypothet
1445 49 10.6 303 1 P3BVM 3a protein - bromo
1446 49 10.6 303 2 S50688 hypothetical prote
1447 49 10.6 318 2 T36262 probable dehydroge
1448 49 10.6 319 2 S55434 conserved hypothet
1449 49 10.6 326 2 B70193 oligopeptide ABC t
1450 49 10.6 333 1 K8RTH cathepsin H (EC 3.
1451 49 10.6 333 1 DCRTDM adenosylmethionine
1452 49 10.6 334 1 DCHUDM adenosylmethionine
1453 49 10.6 335 2 AB0776 probable exported
1454 49 10.6 337 2 T06720 hypothetical prote
1455 49 10.6 343 2 B38257 glucan endo-1,3-be
1456 49 10.6 347 2 T21067 hypothetical prote
1457 49 10.6 348 2 T03739 nitrilase (EC 3.5.
1458 49 10.6 348 2 A55020 recombination prot
1459 49 10.6 351 2 AE1923 c-type cytochrome
1460 49 10.6 354 2 S24352 gustducin - rat
1461 49 10.6 355 2 H71930 probable phospholi
1462 49 10.6 360 2 T37285 collagen dpy-2 - C
1463 49 10.6 362 2 AI0433 trypsin-like prote
1464 49 10.6 368 2 H96990 probable membrane
1465 49 10.6 371 2 D95000 GTP-binding protei
1466 49 10.6 371 2 D97872 conserved hypothet
1467 49 10.6 372 2 T47763 hypothetical prote
1468 49 10.6 379 2 AD3390 p11M protein [limp
1469 49 10.6 380 2 T28888 cuticle collagen d
1470 49 10.6 383 2 A23516 Balbiani ring 1 ch
1471 49 10.6 386 2 T19940 hypothetical prote
1472 49 10.6 388 2 H83692 hypothetical prote
1473 49 10.6 389 2 B86017 probable 3-oxoacyl
1474 49 10.6 389 2 F91171 probable 3-oxoacyl
1475 49 10.6 392 2 T43206 probable aminopept
1476 49 10.6 398 2 AE2769 hypothetical prote
1477 49 10.6 417 2 T20199 hypothetical prote
1478 49 10.6 418 2 S30134 hypothetical prote
1479 49 10.6 420 2 F97549 glutathione-indepe
1480 49 10.6 438 2 E97342 high affinity gluc
1481 49 10.6 446 2 S69051 hypothetical prote
1482 49 10.6 448 2 G87482 acetyl-CoA carboxy
1483 49 10.6 450 2 T04265 probable kasein ki
1484 49 10.6 452 2 D64583 hypothetical prote
1485 49 10.6 456 1 E42594 hypothetical prote
1486 49 10.6 458 2 A48380 tyrosine phenol-ly
1487 49 10.6 459 2 G71619 PINT domain protei
1488 49 10.6 464 2 S75362 hypothetical prote
1489 49 10.6 467 2 T38806 probable aspartyl

mannose-6-phosphat
Ig heavy chain pre
septum formation p
probable glycerol
hypothetical prote
hypothetical prote
nucleocapsid prote
scarecrow-like 7 (
probable rpp-regui
legumin B - fava b
single-stranded DN

ALIGNMENTS

RESULT 1

AE1734

anti-repressor homolog lin2418 [imported] - *Listeria innocua* (strain Clip11262)C:Species: *Listeria innocua*

C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C:Accession: AE1734

R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fshini, H.;

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat

ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,

A:Title: Comparative genomics of *Listeria* species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AE1734

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-256 <GLA>

A:Cross-references: UNIPROT:Q928W4; GB:AL592022; PIDN:CAC97645.1; PID:gl6414940; GSPDB:G

A:Experimental source: strain Clip11262

C:Genetics:

A:Gene: lin2418

Query Match 15.2%; Score 70; DB 2; Length 256;

Best Local Similarity 31.4%; Pred. No. 6.4;

Matches 16; Conservative 8; Mismatches 13; Indels 14; Gaps 1;

QY 27 ENGXYFLSRNKHSHOPTQSSLEDSVTPTK-----AVKTTGKG 63

DB 190 QNGYLIIRRGIDYNRPTQKSMELGLFKETAIMRSSGAHTAITAKVTGKG 240

RESULT 2

S76967

hypothetical protein - *Synechocystis* sp. (strain PCC 6803)C:Species: *Synechocystis* sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C:Accession: S76967

O.; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O.; K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*

s.

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S76967

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-495 <KAN>

A:Cross-references: UNIPROT:Q55897; EMBL:D64005; GB:AB001339; NID:gl001779; PIDN:BAA1065;

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 14.8%; Score 68.5; DB 2; Length 495;

Best Local Similarity 32.3%; Pred. No. 19;

Matches 20; Conservative 7; Mismatches 26; Indels 9; Gaps 2;

QY 21 SGNSTLENGYFLSRNKE-----NHSOPTQSSLEDSVTPTKAVKTTG-KGIVKGRNLD 71

Db
23 SGTSTPTPTGVTIAEVGEQACASTEINQESNQKGETKNPLKVVVSATGVKSVAKGNVG 82

Qy	72 SR 73
D _b	83 LR 84

RESULT 3

A34549

transferrin receptor - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004

C:Accession: A34549

P:Roberts, K.F.; Griswold, M.D.

Mol. Endocrinol. 4, 531-542, 1990

A:Title: Characterization of rat transferrin receptor cDNA: the regulation of transferrin

A:Reference number: A34549; MUID:91125359; PMID:2126342

A:Accession: A34549

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-622 <ROB>

A:Cross-references: UNIPROT:Q99376; GB:M58040; NID:g207463; PIDN:AAA42273.1; PID:g207466

C:Superfamily: transferrin receptor

C:Keywords: receptor; transmembrane protein

Query Match	14.8%	Score 68.5;	DB 2;	Length 622;
Best Local Similarity	27.6%;	Pred. No. 24;		
Matches 21;	Conservative	15;	Mismatches 23;	Indels 17;
				Gaps 3;

[illegible]

QY	77	LGA--EAWGRGVKNT	90
	:		
Db	267	VGAQRDAWPGVAKSS	282

RESULT 4
E82099 phosphatidate cytidyltransferase VC2255 [imported] - Vibrio cholerae (strain N16961 se
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: E82099
R;Reidsberg, J.P.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.
l, R.K.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; PMID:20406833; PMID:10952301

A;Accession: E82099
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-280 <HEI>
A;Cross-references: UNIPROT:Q9KPV7; GB:AE004297; GB:AE003852; NID:g9656810; PIDN:AAF9539
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC2255
A;Map position: 1
C;Superfamily: phosphatidate cytidyltransferase

Query Match 14.7%; Score 68; DB 2; Length 280;
Best Local Similarity 25.3%; Pred. No. 12;
Matches 20; Conservative 17; Mismatches 20; Gaps 4;
Indels 22; Gaps 4;

QY 8 LLLLVCEAIWRNSGNTLENGYFLSRNKHNSOPTQSILEDSTPTKAVKTGKGVKG 67
| : | | : | : | : || : : | : | : | : | : | : | : | : | :
Db 151 LVLFVCFVLVAADSGA-----YFVGKSGLKH-----KWAPVSPNKTEI GLVGVIV-- 196

Qy	68	RNLDSRGLILG---	AEAWG	83
		:	:	:
Db	197	-----TANLVGYWVAECFG		210

RESULT 5

T41524
rhol_gdp-ctp exchange protein 1 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T41524
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.
submitted to the EMBL Data Library, March 1999
A;Reference number: Z22000
A;Accession: T41524

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1334 <MOO>
A;Cross-references: UNIPROT:Q9Y7U6; EMBL:AL049498;
A;Experimental source: strain 972h-; cosmid c645
C;Genetics:
A;Gene: SPDB.SPCC645.07
A;Map position: 3
A;Intons: 894/3
C;Superfamily: GDP/GTP exchange protein ROM1; CDC224

Query Match	14.7%	Score 68;	DB 2;	Length 1334;
Best Local Similarity	21.8%;	Pred. No. 64;		
Matches 12;	Conservative	19;	Mismatches	22;
			Indels	22;
			Gaps	1;

[illegible]

RESULT 6

A83026
 hypotetical protein PA4966 [imported] - Pseudomonas aeruginosa (strain PA01)
 C1:Species: Pseudomonas aeruginosa
 C1:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
 C1:Accession: A83026
 R1:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrner, P.; Hickler,
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbi
 .; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A1:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportun
 A1:Reference number: A82950; PMID:20437337; PMID:10994043

A;Accession: A83026
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-337 <STO>
A;Cross-references: UNIPROT
C;Experimental source:
C;Genetics:
A;Gene: PA4366

Query Match	14.4%	Score 66.5;	DB 2;	Length 337;
Best Local Similarity	25.7%;	Pred. No. 20;		
Matches 19;	Conservative	12;	Mismatches 32;	Indels 11;
				Gaps 2;

QY 15 AIWRNSGSNTIENG YFLSRNKENHSQTQSLSDSVTPT-----KAVTKTGIV 65
| | : : | : | | | : | : | : | : | : | : | : | : | : | : |
Db 55 ALWTVSDRDD--DRRLRPLPSAEGSDPWAQAESEFIAPPPDGLPWGNSTRVMT.SGLV 112

QY	66	KGRN	DSRG	LILGA	79
	:				:
Db	113	RGNL	DFEG	IA CDA	12

RESULT 7

S41015
transcription factor tbx8 - Caenorhabditis elegans
NAlternate names: hypothetical protein T07C4.2
C.Species: Caenorhabditis elegans
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
C.Accession: S41015; A56530

R.Berks, M.
submitted to the EMBL Data Library, January 1994
A:Reference number: S41014
A:Accession: S41015
A:Molecule type: DNA
A:Residues: 1-479 <BER>
A:Cross-references: EMBL:Z29443
R:Agulnik, S.I.; Bollag, R.J.; Silver, L.M.
Genomics 25, 214-219, 1995
A:Title: Conservation of the T-box gene family from *Mus musculus* to *Caenorhabditis elegans*
A:Reference number: A56530; MUID:95293375; PMID:7774921
A:Accession: A56530
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 153-340 <AGU>
A:Cross-references: GB:Z29443
C:Genetics:
A:Introns: 77/3; 101/3; 134/3; 236/2; 261/3; 312/3; 450/3
C:Superfamily: *Caenorhabditis elegans* transcription factor tbx8; T-box homology
C:Keywords: DNA binding
F:153-340/Domain: T-box homology <TBX>

Query Match 14.4%; Score 66.5; DB 1; Length 479;
Best Local Similarity 25.0%; Pred.No.30;
Matches 18; Conservative 13; Mismatches 22; Indels 19; Gaps 3;

QY 19 SNSGNSLLENGYFLSRNKENHSOFTQSLEDSVTPTKAVAKTTGKGVKGNLDSRGLILG 78
DB 85 AHGASNT-----NKINQNLSP-HPAKHKTTPTSVIATVPRGPPSGR----- 126
:: |||::
:: |||::

QY 79 AEAMGRGVKNT 90
DB 127 -QEWGRGIQRT 137
: |||::
: |||::

RESULT 8
T47495
hypothetical protein F9K21.l30 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T47495
R:Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Lemcke, K.
submitted to the Protein Sequence Database, February 2000
A:Reference number: Z24467
A:Accession: T47495
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-851 <JOR>
A:Cross-references: UNIPROT:Q9M1F2; EMBL:AL138657
A:Experimental source: cultivar Columbia; BAC clone F9K21
C:Genetics:
A:Map position: 3
A:Note: F9K21.l30

Query Match 14.3%; Score 66; DB 2; Length 851;
Best Local Similarity 25.6%; Pred.No.64;
Matches 20; Conservative 13; Mismatches 23; Indels 22; Gaps 2;

QY 16 IWSNS-GSNTLENGYFLSRNKENHSOFTQSLEDSV-----TP 53
DB 625 IWSYNTGDTYVRSGYWLSTHDPSTNTIPTMAKPHGSVDLTKIWNLPIMPXKHLFWRL 684
:: |||::
:: |||::

QY 54 TKAVKTTGKGVKGNLD 71
DB 685 SKALPTDRLTRGMRIID 702
:: |||::
:: |||::

RESULT 9
A82436
transcription regulator LysR family VCA0635 [imported] - *Vibrio cholerae* (strain N16961)
C:Species: *Vibrio cholerae*
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: A82436

[illegible]

RESULT 11
S36576
E2 protein - human papillomavirus type 52
C/Species: human papillomavirus type 52
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C/Accession: S36576
R/Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A/Description: Primer-directed sequencing of human papillomavirus types.
A/Reference number: S36469
A/Accession: S36576
A/Molecule type: DNA
A/Residues: 1-368
A/Cross-references: UNIPROT:P36796; EMBL:X74481; NID:q397038; PIDN:CAAS2588.1; PID:q39704

```
C;Superfamily: papillomavirus E2 protein
C;Keywords: DNA binding; early protein; transcription regulation

Query Match      14.1%; Score 65; DB 2; Length 368;
Best Local Similarity 27.0%; Pred. No. 32;
Matches 24; Conservative 11; Mismatches 40; Indels 14; Gaps 3;

QY 10 LLYCEAIWRNSGSGNTLENGYFLSRN-----KENHSOPTQSSLEDSVTPTKAVK 58
Db 192 VIVCPASVSNEVSTT-ETAVHLCTETSKTSVSGVGAOKTHLQPPQRRRPDVTDSRNTK 250

QY 59 TTQKGIVKGNLDS--RGLILGAEAMGRG 85
Db 251 YPNMLLRGQOSVDSITRGLVTATECTNKG 279

RESULT 12
T24654
Hypothetical protein T07D10.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24654
R;White, S.
Submitted to the EMBL Data Library, November 1996
A;Reference number: Z19918
A;Accession: T24654
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-379 <WIL>
A;Cross-references: UNIPROT:O02300; EMBL:Z81588; PIDN:CAB04712.1; GSPDB:GN000019; CESP:T07D10
A;Experimental source: clone T07D10
C;Genetics:
A;Gene: CESP:T07D10.2
A;Map position: 1
A;Introns: 37/3; 85/3; 271/1; 319/1
C;Superfamily: oxytocin receptor

Query Match      14.1%; Score 65; DB 2; Length 379;
Best Local Similarity 35.9%; Pred. No. 34;
Matches 14; Conservative 9; Mismatches 12; Indels 4; Gaps 1;

QY 8 LLLVCEAIWRNSGSGNTLENGYFLSRNKENHSOPTQSS 46
Db 228 LXLVCVCKAVKMTSPFSSLRN----NKKRMEHMKLTEKN 262

RESULT 13
T06029
Hypothetical protein T28I19.100 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cross)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C;Accession: T06029
R;Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, G.; Ba
Submitted to the Protein Sequence Database, March 1999
A;Reference number: Z15484
A;Accession: T06029
A;Molecule type: DNA
A;Residues: 1-532 <BEV>
A;Cross-references: UNIPROT:Q9T069; EMBL:AL035709; GSPDB:GN000062; ATSP:T28I19.100
A;Experimental source: cultivar Columbia; BAC clone T28I19
C;Genetics:
A;Gene: ATSP:T28I19.100
A;Map position: 4

Query Match      14.0%; Score 64.5; DB 2; Length 532;
Best Local Similarity 34.7%; Pred. No. 55;
Matches 17; Conservative 9; Mismatches 18; Indels 5; Gaps 1;

QY 14 EAIMRNSGSGNTLENGYFLSRNKENHSOPTQSSLEDSVTPTKAVKTTGK 62
Db 274 ESSGSGDESGSGKSTGYCQTKNEDEKVKQSSBEES-----KVKESGK 317
```

```
RESULT 14
A11442
anti-repressor (Bacteriophage A118) homolog lin0080 [imported] - Listeria innocua (stra
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: A11442
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Feihl, H
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tietze, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland
A;Title: Comparative genomics of Listeria species
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: A11442
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-257 <GLA>
A;Cross-references: UNIPROT:Q92FM4; GB:AL592022; PIDN:CAC95313.1; PID:gl16412500; GSPDB:
A;Experimental source: strain Clp11262
C;Genetics:
A;Gene: lin0080

Query Match      13.9%; Score 64; DB 2; Length 257;
Best Local Similarity 29.4%; Pred. No. 28;
Matches 15; Conservative 8; Mismatches 14; Indels 14; Gaps 1;

QY 27 ENGYFLSRNKENHSOPTQSSLEDSVTPTK-----AVKTKGK 63
Db 191 QRGYLISRKGTQDYNRPTQKMBELGLFKIKETAIIRSSGAQTAKVTGK 241

RESULT 15
T46099
Hypothetical protein T25B15.60 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cross)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T46099
R;Alcaraz, J.P.; Clabault, G.; Cottet, A.; Mache, R.; Mewes, H.W.; Lemcke, K.; Mayer, K
Submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23021
A;Accession: T46099
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-430 <ALC>
A;Cross-references: UNIPROT:Q9FT53; EMBL:AL132972
A;Experimental source: cultivar Columbia; BAC clone T25B15
C;Genetics:
A;Map position: 3
A;Introns: 23/3; 122/3; 194/3; 234/3
A;Note: T25B15.60
C;Superfamily: Arabidopsis thaliana hypothetical protein T16L24.240

Query Match      13.9%; Score 64; DB 2; Length 430;
Best Local Similarity 27.4%; Pred. No. 49;
Matches 20; Conservative 14; Mismatches 23; Indels 16; Gaps 3;

QY 17 WRSNS--GSNT-----LENGYFLSRNKENHSOPTQSSLEDSVTPTKAVKTTG 61
Db 237 WKNSTKMGSGTQFMDPNPNHGWGWSWLER-WMAARPENHSLTPDNAEKDSSARSVASRAMS 295

QY 62 KGIVKGNLDSRG 74
Db 296 EMIPRGNLSPRG 308

Search completed: November 30, 2004, 14:43:09
Job time : 16 secs
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OM protein - protein search, using sw model

Run on: November 30, 2004, 14:42:45 ; Search time 44 Seconds
(without alignments)
1176.903 Million cell updates/sec

Title: US-09-997-653-377

Perfect score: 462

Sequence: 1 MTFPLSLLLLVCEAIWRSN.....DSRGLILGAEGRWGVKKNT 90

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	462	100.0	90	2 Q6UWR2	Q6UWR2 homo sapien
2	462	100.0	90	2 AAc89048	AAc89048 homo sapien
3	247.5	53.6	189	2 Q96DR9	Q96DR9 homo sapien
4	247.5	53.6	192	2 Q96PAS	Q96PAS homo sapien
5	247.5	53.6	247	2 Q9BXN2	Q9BXN2 homo sapien
6	217.5	47.1	247	2 Q8HZR8	Q8HZR8 macaca mula
7	143.5	31.1	244	2 Q6QLQ4	Q6QLQ4 mus musculus
8	143.5	31.1	244	2 Q9J150	Q9J150 mus musculus
9	143.5	31.1	244	2 AAc37670	AAc37670 mus musculus
10	136.5	29.5	244	2 Q8K1L4	Q8K1L4 mus musculus
11	80	17.3	239	2 Q8NZP4	Q8NZP4 streptococc
12	80	17.3	242	2 Q79XW8	Q79XW8 streptococc
13	80	17.3	242	2 Q938N5	Q938N5 temperate p
14	78	16.9	238	2 Q48311	Q48311 streptococc
15	77	16.7	287	2 Q38585	Q38585 streptococc
16	75	16.2	217	2 Q8S2U4	Q8S2U4 medicago sa
17	74	16.0	369	2 Q6C2Z3	Q6C2Z3 yarrowia li
18	73	15.8	311	2 Q6DHT6	Q6DHT6 brachydanio
19	71	15.4	213	2 Q9SBR7	Q9SBR7 medicago va
20	70	15.2	205	2 Q8PDR9	Q8PDR9 xanthomonas
21	70	15.2	256	2 Q9Z8W4	Q9Z8W4 listeria in
22	70	15.2	621	2 Q7KSM9	Q7KSM9 drosophila
23	70	15.2	621	2 AAc65142	AAc65142 drosophil
24	70	15.2	661	2 Q9VG84	Q9VG84 drosophila
25	70	15.2	696	2 Q8MZC0	Q8MZC0 drosophila
26	69.5	15.0	253	2 Q6SEFA	Q6SEFA lactobacill
27	69.5	15.0	253	2 AAr27357	AAr27357 lactobaci
28	69.5	15.0	253	2 AAc09223	AAc09223 lactobaci
29	69.5	15.0	265	2 Q8NC54	Q8NC54 homo sapien
30	69.5	15.0	265	2 Q9NRG2	Q9NRG2 homo sapien
31	69	14.9	1577	2 Q6NVJ5	Q6NVJ5 brachydanio

32	69	14.9	1577	2	AAH68015	AAh68015 brachydan
33	68.5	14.8	495	2	Q55897	Q55897 synechocyst
34	68.5	14.8	505	2	Q6K4U9	Q6K4U9 oryza sativ
35	68.5	14.8	622	1	TFRL_RAT	Q93376 rattus norv
36	68.5	14.8	4498	2	Q93291	Q93291 fugu rubrip
37	68	14.7	115	2	Q7PMB6	Q7pmb6 anopheles g
38	68	14.7	280	2	Q9KPV7	Q9kpv7 vibrio chol
39	68	14.7	1008	2	Q72RJ0	Q72rj0 leptospira
40	68	14.7	1008	2	Q8F478	Q8f478 leptospira
41	68	14.7	1008	2	AA570344	AA570344 leptospir
42	68	14.7	1334	2	Q9Y7U6	Q9y7u6 schizosacch
43	68	14.7	2621	2	Q7P5V6	Q7p5v6 fusobacteri
44	67.5	14.6	198	2	Q6WU72	Q6wu72 lactobacill
45	67.5	14.6	198	2	AAp97070	AAp97070 lactobaci
46	67.5	14.6	417	2	Q8LAR3	Q8lar3 arabidopsis
47	67	14.5	150	2	Q9D851	Q9d851 m mus muscu
48	67	14.5	226	1	R85_MYCGA	Q52349 mycoplasma
49	67	14.5	321	2	Q6NXX5	Q6nxx5 mus musculu
50	67	14.5	321	2	Q8BTR4	Q8btr4 m mus muscu
51	67	14.5	321	2	AAH67028	AAh67028 mus muscu
52	67	14.5	356	2	Q57435	Q57435 fugu rubrip
53	67	14.5	976	2	Q862D2	Q862d2 drosophila
54	67	14.5	976	2	Q8INT1	Q8int1 drosophila
55	66.5	14.4	337	2	Q9HUJ9	Q9huJ9 pseudomonas
56	66.5	14.4	574	2	Q7SHJ5	Q7shj5 neurospora
57	66.5	14.4	602	2	Q7XBV7	Q7xbv7 oryza sativ
58	66.5	14.4	602	2	Q8M3H4	Q8m3h4 oryza sativ
59	66.5	14.4	738	2	Q6DFA9	Q6dfa9 xenopus lae
60	66.5	14.4	796	2	Q6DDR0	Q6ddr0 xenopus lae
61	66	14.3	145	2	Q8AZ80	Q8az80 influenza a
62	66	14.3	145	2	Q8AZ81	Q8az81 influenza a
63	66	14.3	145	2	Q8AZ82	Q8az82 influenza a
64	66	14.3	145	2	Q8AZ83	Q8az83 influenza a
65	66	14.3	145	2	Q8AZ84	Q8az84 influenza a
66	66	14.3	260	2	Q919W1	Q919w1 influenza a
67	66	14.3	279	1	CH1_CAEBL	Q96618 caenorhabdi
68	66	14.3	417	2	Q9SFE3	Q9sfe3 arabidopsis
69	66	14.3	491	2	Q919W0	Q919w0 influenza a
70	66	14.3	491	2	Q919W2	Q919w2 influenza a
71	66	14.3	498	2	Q92607	Q92607 influenza a
72	66	14.3	498	2	Q75T93	Q75t93 influenza a
73	66	14.3	498	2	Q75TA3	Q75ta3 influenza a
74	66	14.3	498	2	Q77Y46	Q77y46 influenza a
75	66	14.3	498	2	Q8AZ75	Q8az75 influenza a
76	66	14.3	498	2	Q8B674	Q8b674 influenza a
77	66	14.3	498	2	Q8B675	Q8b675 influenza a
78	66	14.3	498	2	Q8B676	Q8b676 influenza a
79	66	14.3	498	2	Q8B677	Q8b677 influenza a
80	66	14.3	498	2	Q9YIL3	Q9yil3 influenza a
81	66	14.3	498	2	Q9QNB4	Q9qnb4 influenza a
82	66	14.3	498	2	Q9QNB5	Q9qnb5 influenza a
83	66	14.3	498	2	Q995P9	Q995p9 influenza a
84	66	14.3	498	2	Q8QM08	Q8qm08 influenza a
85	66	14.3	498	2	BAD02348	BAD02348 influenza
86	66	14.3	498	2	BAD02358	BAD02358 influenza
87	66	14.3	851	2	Q9M1F2	Q9m1f2 arabidopsis
88	65.5	14.2	274	2	Q72QR3	Q72qr3 leptospira
89	65.5	14.2	274	2	AA570621	AA570621 leptospir
90	65.5	14.2	370	2	Q9FB13	Q9fb13 streptococ
91	65.5	14.2	499	2	Q86ZN9	Q86zn9 fusarium ox
92	65.5	14.2	544	2	Q87BG8	Q87bg8 xylella fas
93	65.5	14.2	706	2	Q8F5C4	Q8f5c4 leptospira
94	65	14.1	242	2	Q9A036	Q9a036 streptococc
95	65	14.1	253	2	Q8P1S9	Q8pls9 streptococc
96	65	14.1	265	2	Q6R854	Q6r854 bacteriopho
97	65	14.1	265	2	Q9MBT0	Q9mbt0 staphylococ
98	65	14.1	265	2	AA87882	AA87882 bacteriop
99	65	14.1	313	2	Q9KLV6	Q9klv6 vibrio chol
100	65	14.1	360	2	Q97DV3	Q97dv3 clostridium
101	65	14.1	368	1	V52_HPVS0	P36796 human papil
102	65	14.1	379	2	Q02300	Q02300 caenorhabdi
103	65	14.1	452	2	Q8CML9	Q8cml9 staphylococ
104	65	14.1	583	2	Q6BUP6	Q6bup6 debaryomyce

105	65	14.1	1164	2	Q8PRX0	Q8prx0 methanosarc	178	63	13.6	533	2	AAR26936	Aar26936 feldmanni
106	65	14.1	2858	2	Q8IAK2	Q8iak2 plasmodium	179	63	13.6	586	2	Q893I7	Q893i7 clostridium
107	64.5	14.0	339	2	Q82IP9	Q82ip9 streptomyces	180	63	13.6	616	2	Q8NI84	Q8ni84 homo sapien
108	64.5	14.0	338	2	Q7NU10	Q7nj10 gloeobacter	181	63	13.6	642	2	Q8DHT6	Q8dht6 yaba-like d
109	64.5	14.0	360	2	Q6LZ29	Q6lhz29 methanococ	182	63	13.6	671	1	SP20 MOUSE	Q8rix6 mus musculu
110	64.5	14.0	360	2	CAF30356	Caf30356 methanococ	183	63	13.6	808	2	Q6Q8T1	Q6q8t1 uncultured
111	64.5	14.0	468	2	Q7U7N7	Q7u7n7 synechococ	184	63	13.6	808	2	AAS73136	Aas73136 unculture
112	64.5	14.0	523	2	Q7W6U2	Q7w6u2 bordetella	185	63	13.6	895	2	Q82MF3	Q82mf3 streptomyce
113	64.5	14.0	532	2	Q9T069	Q9t069 arabidopsis	186	63	13.6	993	2	P92030	P92030 drosophila
114	64.5	14.0	539	2	Q75CV9	Q75cv9 ashbya goss	187	63	13.6	1004	2	Q7YU43	Q7yu43 drosophila
115	64.5	14.0	539	2	AAS51035	Aas51035 ashbya go	188	63	13.6	1020	2	Q8CCW3	Q8ccw3 mus musculu
116	64.5	14.0	562	2	Q8TH3	Q8th3 drosophila	189	63	13.6	1059	2	Q9VQ47	Q9vq47 drosophila
117	64.5	14.0	781	2	Q7PLI0	Q7pli0 drosophila	190	63	13.6	1101	2	Q7KU08	Q7ku08 drosophila
118	64.5	14.0	781	2	Q9NHP1	Q9nhp1 drosophila	191	63	13.6	1101	2	AAS64628	Aas64628 drosophil
119	64.5	14.0	1295	2	Q75BP7	Q75bp7 ashbya goss	192	63	13.6	2425	2	O28859	O28859 archaeoglob
120	64.5	14.0	1295	2	AAS51450	Aas51450 ashbya go	193	63	13.6	3071	2	Q8QXL2	Q8qx12 sorghum mos
121	64.5	14.0	1590	2	Q6BUJ1	Q6bje1 debaryomyce	194	62.5	13.5	124	2	Q8AZ77	Q8az77 influenza a
122	64	13.9	255	1	RR3_CHAGL	Q8m9v0 chaetosphae	195	62.5	13.5	128	2	Q8B3F7	Q8b3f7 influenza a
123	64	13.9	257	2	Q92FM4	Q92fm4 listeria in	196	62.5	13.5	128	2	Q8B3F8	Q8b3f8 influenza a
124	64	13.9	376	2	Q9QB25	Q9qb25 human adeno	197	62.5	13.5	128	2	Q8B3F9	Q8b3f9 influenza a
125	64	13.9	381	2	Q8TMI0	Q8tmi0 methanosarc	198	62.5	13.5	128	2	Q8B3G0	Q8b3g0 influenza a
126	64	13.9	430	2	Q9FT53	Q9ft53 arabidopsis	199	62.5	13.5	128	2	Q8B3G1	Q8b3g1 influenza a
127	64	13.9	507	2	Q82VU0	Q82vj0 nitrosomona	200	62.5	13.5	128	2	Q8B3G2	Q8b3g2 influenza a
128	64	13.9	548	2	Q22809	Q22809 caenorhabdi	201	62.5	13.5	128	2	Q8B3G3	Q8b3g3 influenza a
129	64	13.9	627	2	Q87YS0	Q87ys0 pseudomonas	202	62.5	13.5	128	2	Q8B3G4	Q8b3g4 influenza a
130	64	13.9	1062	2	Q7V8G6	Q7veg6 prochloroco	203	62.5	13.5	128	2	Q8B3G5	Q8b3g5 influenza a
131	64	13.9	1066	2	Q6CU73	Q6cu73 kluyveromyc	204	62.5	13.5	219	2	Q6WI53	Q6wi53 bacterioph
132	64	13.9	1189	2	Q86ZA8	Q86za8 cochlribolu	205	62.5	13.5	219	2	AAQ64170	AAq64170 bacteriop
133	64	13.9	1570	2	Q8DX06	Q8dx06 streptococ	206	62.5	13.5	268	1	PYRF PACTA	P93864 pachysolen
134	64	13.9	1570	2	Q8E2V6	Q8e2v6 streptococ	207	62.5	13.5	270	2	Q81F78	Q81f78 bacillus ce
135	64	13.9	1656	2	Q9Y474	Q9y474 homo sapien	208	62.5	13.5	295	2	Q96NB0	Q96nb0 homo sapien
136	63.5	13.7	254	2	Q6J1W3	Q6j1w3 bacterioph	209	62.5	13.5	363	2	Q72UC0	Q72uc0 leptospira
137	63.5	13.7	254	2	AAT36510	Aat36510 bacteriop	210	62.5	13.5	363	2	Q8FOQ8	Q8foq8 leptospira
138	63.5	13.7	284	2	Q9W4U0	Q9w4u0 drosophila	211	62.5	13.5	363	2	AAS69358	Aas69358 leptospir
139	63.5	13.7	585	2	Q896P7	Q896p7 clostridium	212	62.5	13.5	364	2	Q18093	Q18093 caenorhabdi
140	63.5	13.7	591	2	Q6N044	Q6n044 homo sapien	213	62.5	13.5	371	2	Q87LY5	Q87ly5 vibrio para
141	63.5	13.7	591	2	CAE45826	Caes45826 homo sapi	214	62.5	13.5	371	2	Q6DCH5	Q6dch5 xenopus lae
142	63.5	13.7	598	2	O25315	O25315 helicobacte	215	62.5	13.5	379	1	Y528_SYNY3	O55518 synchocyst
143	63.5	13.7	651	2	Q8C9Q4	Q8c9q4 arabidopsis	216	62.5	13.5	400	2	Q95G12	Q95g12 aristolochi
144	63.5	13.7	669	1	CALC_HUMAN	F54803 homo sapien	217	62.5	13.5	404	2	Q9V4W2	Q9v4w2 drosophila
145	63.5	13.7	669	2	Q8UJ030	Q8uj030 homo sapien	218	62.5	13.5	510	2	Q7PZG8	Q7pzg8 anopheles g
146	63.5	13.7	705	1	CDC5_YEAST	P32562 saccharomyc	219	62.5	13.5	584	2	O45Q30	O45q30 drosophila
147	63.5	13.7	719	2	Q8VL77	Q8vl77 treponema d	220	62.5	13.5	617	2	Q8UC83	Q8uc83 agrobacteri
148	63.5	13.7	722	2	P96091	P96091 treponema d	221	62.5	13.5	641	2	Q7CWM5	Q7cwm5 agrobacteri
149	63.5	13.7	818	2	Q86XP0	Q86xp0 homo sapien	222	62.5	13.5	682	2	Q6FLM0	Q6flm0 mesoplasma
150	63.5	13.7	837	1	SLK4_HUMAN	Q8iw52 homo sapien	223	62.5	13.5	725	2	Q965E8	Q965e8 entamoeba h
151	63.5	13.7	850	2	Q34411	Q43411 brasica ol	224	62.5	13.5	849	2	Q43393	Q43393 brassica na
152	63.5	13.7	882	1	KEL2_YEAST	P50090 saccharomyc	225	62.5	13.5	1123	2	Q8YVR0	Q8yvr0 anabaena sp
153	63.5	13.7	1233	2	Q6ZU35	Q6zu35 homo sapien	226	62.5	13.5	1553	2	Q77385	Q77385 plasmodium
154	63.5	13.7	1233	2	BAC86392	Bac86392 homo sapi	227	62.5	13.5	1859	2	Q8IC27	Q8ic27 plasmodium
155	63	13.6	80	1	DMS6_AGAAN	Q93226 agalychnis	228	62.5	13.5	1998	2	Q6CSW6	Q6csw6 kluyveromyc
156	63	13.6	138	2	Q8AZ76	Q8az76 influenza a	229	62.5	13.5	2025	2	Q8UTZ4	Q8utz4 lumpy skin
157	63	13.6	186	2	Q7YXH0	Q7yxh0 caenorhabdi	230	62.5	13.5	2025	2	Q9JMN0	Q9jmn0 lumpy skin
158	63	13.6	249	2	O80074	O80074 staphylococ	231	62	13.4	84	2	Q9JMR3	Q9jmr3 neisseria m
159	63	13.6	249	2	Q8SDM9	Q8sdm9 staphylococ	232	62	13.4	84	2	P74D18	P74dd18 neisseria m
160	63	13.6	249	2	Q8NMV6	Q8nmv6 staphylococ	233	62	13.4	149	2	P74633	P74633 synchocyst
161	63	13.6	249	2	Q6R850	Q6r850 bacterioph	234	62	13.4	194	2	Q7QJP3	Q7qip3 anopheles g
162	63	13.6	250	2	Q9G034	Q9g034 bacterioph	235	62	13.4	289	2	Q8ESK4	Q8esk4 oceanobacil
163	63	13.6	250	2	Q6GR60	Q6gr60 staphylococ	236	62	13.4	337	2	Q86Z41	Q86z41 leptosphaer
164	63	13.6	250	2	Q99SP8	Q99sp8 staphylococ	237	62	13.4	407	2	Q8PBN2	Q8pbn2 acinetobact
165	63	13.6	250	2	AAR87886	Aar87886 bacteriop	238	62	13.4	583	2	Q8PZC2	Q8pzc2 methanosarc
166	63	13.6	251	2	Q31J74	Q31j74 staphylococ	239	62	13.4	649	2	Q6ZBS6	Q6zbs6 oryza sativ
167	63	13.6	260	2	Q6TVN2	Q6tvn2 orf virus	240	62	13.4	649	2	BAD03041	Bad03041 oryza sat
168	63	13.6	260	2	AAR98313	Aar98313 orf virus	241	62	13.4	649	2	BAD03237	Bad03237 oryza sat
169	63	13.6	273	2	Q8CRN8	Q8crn8 staphylococ	242	62	13.4	708	2	Q7SCB5	Q7scb5 ashbya goss
170	63	13.6	341	2	Q8SU44	Q8su44 encephalito	243	62	13.4	708	2	AAS51222	Aas51222 ashbya go
171	63	13.6	441	2	O23053	O23053 arabidopsis	244	62	13.4	768	2	Q8HZV3	Q8hzv3 sus scrofa
172	63	13.6	441	2	Q8L738	Q8l738 arabidopsis	245	62	13.4	1017	2	O74670	O74670 pneumocysti
173	63	13.6	457	2	Q9MAI3	Q9mai3 arabidopsis	246	62	13.4	1022	2	O74671	O74671 pneumocysti
174	63	13.6	491	2	Q725L9	Q725l9 desulfovibr	247	62	13.4	1026	2	O74669	O74669 pneumocysti
175	63	13.6	491	2	AAS97664	Aas97664 desulfovi	248	62	13.4	1351	2	Q6FKP1	Q6fkp1 candida gla
176	63	13.6	508	2	Q9BLR4	Q9blr4 leishmania	249	62	13.4	1634	1	DPOL_METJA	D98295 methanococ
177	63	13.6	533	2	Q6XIX5	Q6xix5 feldmannia	250	62	13.4	2075	2	Q9VXY2	Q9vxy2 drosophila

251	62	13.4	2541	2	Q7QSH8	Q7qsh8 giardia lam	324	60.5	13.1	194	2	Q8SJE1	Q8sje1 helobdella
252	61.5	13.3	146	2	Q8VQ11	Q8vq11 uncultured	325	60.5	13.1	195	2	Q8SJF0	Q8sjf0 helobdella
253	61.5	13.3	156	2	Q6TGP8	Q6tgp8 xanthoria p	326	60.5	13.1	195	2	Q8SJF2	Q8sjf2 helobdella
254	61.5	13.3	156	2	AA575133	AA575133 xanthoria	327	60.5	13.1	195	2	Q8SJF7	Q8sjf7 helobdella
255	61.5	13.3	195	2	Q8SJF4	Q8sjf4 helobdella	328	60.5	13.1	221	2	Q25140	Q25140 helobdella
256	61.5	13.3	266	2	Q748H4	Q748h4 helobacter s	329	60.5	13.1	222	2	Q9FX28	Q9fx28 arabidopsis
257	61.5	13.3	266	2	Q748H4	Q748h4 helobacter s	330	60.5	13.1	262	2	Q89PD9	Q89pd9 bradyrhizob
258	61.5	13.3	266	2	Q748H4	Q748h4 helobacter s	331	60.5	13.1	262	2	Q6HKG9	Q6hkg9 bacillus th
259	61.5	13.3	395	2	Q78752	Q78752 schizosacch	332	60.5	13.1	270	2	Q81S92	Q81s92 bacillus an
260	61.5	13.3	401	1	TRM1_AERPE	Q9ydy7 aeropyrum p	333	60.5	13.1	270	2	AA330891	AA330891 bacillus
261	61.5	13.3	402	2	Q28681	Q28681 oryctolagus	334	60.5	13.1	312	2	Q9MNJ6	Q9mnj6 helobdella
262	61.5	13.3	461	2	Q84PC8	Q84pc8 oryza sativ	335	60.5	13.1	317	2	Q13940	Q13940 homo sapien
263	61.5	13.3	500	2	Q7MOM9	Q7mom9 prevotella	336	60.5	13.1	317	2	AA52759	AA52759 homo sapi
264	61.5	13.3	516	1	MEFA_XENLA	Q03414 xenopus lae	337	60.5	13.1	326	2	Q89710	Q89710 clostridium
265	61.5	13.3	516	2	Q7ZX04	Q7zx04 xenopus lae	338	60.5	13.1	345	2	Q6DJM5	Q6djm5 xenopus lae
266	61.5	13.3	516	2	Q9PFS9	Q9psd9 xenopus lae	339	60.5	13.1	410	2	Q9X039	Q9x039 thermotoga
267	61.5	13.3	566	2	Q8G5R7	Q8g5r7 bifidobacte	340	60.5	13.1	428	2	Q8T3S9	Q8t3s9 cryptobact
268	61.5	13.3	581	2	Q8MRA6	Q8mra6 drosophila	341	60.5	13.1	442	2	Q7RQS2	Q7rqs2 plasmodium
269	61.5	13.3	581	2	Q9V533	Q9v533 drosophila	342	60.5	13.1	449	2	Q8ZTA2	Q8zta2 pyrobaculum
270	61.5	13.3	602	2	Q3MA67	Q3ma67 arabidopsis	343	60.5	13.1	475	2	Q6G5J7	Q6g5j7 bartonella
271	61.5	13.3	644	2	Q3FMI7	Q3fm17 arabidopsis	344	60.5	13.1	498	2	Q90MM1	Q90mm1 human immun
272	61.5	13.3	668	2	Q9MAS1	Q9mas1 arabidopsis	345	60.5	13.1	532	2	Q8I3N0	Q8i3n0 plasmodium
273	61.5	13.3	744	2	Q7RMU8	Q7rmu8 plasmodium	346	60.5	13.1	567	1	TGR2_RAT	TGR238 rattus norv
274	61.5	13.3	759	2	Q934H9	Q934h9 haemophilus	347	60.5	13.1	571	2	Q6L5E7	Q6l5e7 oryza sativ
275	61.5	13.3	789	2	Q715L2	Q715l2 bacillus th	348	60.5	13.1	571	2	AA339158	AA339158 oryza sat
276	61.5	13.3	834	1	CFMF_SCHPO	AA012340 bacillus	349	60.5	13.1	572	2	Q98QE4	Q98qe4 mycoplasma
277	61.5	13.3	960	1	YMK6_YEAST	Q9p6r9 schizosacch	350	60.5	13.1	619	2	Q8ALQ7	Q8alq7 bacteroides
278	61.5	13.3	1324	2	Q7LBC2	Q04279 saccharomyc	351	60.5	13.1	654	2	Q9UTA7	Q9uta7 schizosacch
279	61.5	13.3	1328	2	Q9LBC8	Q9lbc2 helicobacte	352	60.5	13.1	667	2	Q7Z4K0	Q7z4k0 homo sapien
280	61.5	13.3	4868	2	Q91319	Q91319 rana catesb	353	60.5	13.1	676	1	RLM1_YEAST	RLM12224 saccharomyc
281	61	13.2	66	2	Q3IF11	Q91f11 human immun	354	60.5	13.1	699	2	Q9MAH1	Q9mah1 arabidopsis
282	61	13.2	109	2	Q42385	Q42385 hippastrum	355	60.5	13.1	708	1	ICAL_HUMAN	ICAL20810 homo sapien
283	61	13.2	145	2	Q42385	Q42385 hippastrum	356	60.5	13.1	798	2	Q9U4E1	Q9u4e1 oxytricha n
284	61	13.2	216	2	Q8N176	Q8n176 homo sapien	357	60.5	13.1	856	2	Q8P151	Q8p151 dictyosteli
285	61	13.2	217	2	Q8GEM7	Q8gem7 uncultured	358	60.5	13.1	864	2	AAH12791	AAH12791 homo sapi
286	61	13.2	237	1	T4S3_HUMAN	P19075 homo sapien	359	60.5	13.1	882	2	Q8HXX1	Q8hxx1 microptamo
287	61	13.2	242	2	Q8TM13	Q8tm13 methanosarc	360	60.5	13.1	926	2	Q8R554	Q8r554 mus musculus
288	61	13.2	258	2	Q8DSX6	Q8dsx6 streptococc	361	60.5	13.1	953	2	Q8EV30	Q8ev30 pasteurella
289	61	13.2	277	2	Q8V7H3	Q8v7h3 tt virus. o	362	60.5	13.1	1231	2	Q9SK98	Q9sk98 arabidopsis
290	61	13.2	279	2	Q7DJE7	Q7dje7 streptomyce	363	60.5	13.1	1264	2	Q9W0S1	Q9w0s1 drosophila
291	61	13.2	279	2	Q929H3	Q929h3 streptomyce	364	60.5	13.1	1345	2	Q6ZS01	Q6zs01 homo sapien
292	61	13.2	309	2	Q73PP6	Q73pp6 treponema d	365	60.5	13.1	1345	2	BAC87155	BAC87155 homo sapi
293	61	13.2	309	2	AA511243	AA511243 treponema	366	60.5	13.1	1369	1	NFAS_CHICK	NFAS2414 gallus gall
294	61	13.2	332	2	Q70D56	Q70d56 xenopus tro	367	60.5	13.1	1556	2	Q83NF7	Q83nf7 tropheryma
295	61	13.2	332	2	CAE51387	CAE51387 xenopus t	368	60.5	13.1	1571	2	Q8GCW3	Q8gcw3 streptococc
296	61	13.2	363	2	Q7Q254	Q7q254 anopheles g	369	60.5	13.1	1624	2	Q7Z3L7	Q7z3l7 homo sapien
297	61	13.2	368	2	Q7SGK0	Q7sgk0 neurospora	370	60.5	13.1	1668	2	Q7RKA8	Q7rka8 plasmodium
298	61	13.2	382	2	P91703	P91703 drosophila	371	60.5	13.1	1744	2	Q9R095	Q9r095 rattus norv
299	61	13.2	386	2	Q7QRC9	Q7qrc9 giardia lam	372	60.5	13.1	1969	1	Z292_HUMAN	Z292281 homo sapien
300	61	13.2	415	1	B2AR_MACMU	Q28509 macaca mula	373	60.5	13.1	2048	2	Q86JW3	Q86jw3 dictyosteli
301	61	13.2	463	2	Q75H05	Q75h05 oryza sativ	374	60.5	13.1	2213	2	Q6BW03	Q6bw03 debaryomyce
302	61	13.2	463	2	AA579750	AA579750 oryza sat	375	60.5	13.1	2298	1	CU05_HUMAN	CU053r5 homo sapien
303	61	13.2	463	2	AA380333	AA380333 oryza sat	376	60.5	13.1	3531	2	Q7N1Z0	Q7n1z0 photorhabdu
304	61	13.2	498	2	Q8AZ74	Q8az74 influenza a	377	60.5	13.1	99	2	Q8PYA3	Q8pya3 methanosarc
305	61	13.2	519	2	Q91UM4	Q91um4 synecococc	378	60	13.0	174	2	Q6P534	Q6p534 homo sapien
306	61	13.2	548	2	Q939K6	Q939k6 propionibac	379	60	13.0	174	2	AAH63107	AAH63107 homo sapi
307	61	13.2	561	2	Q9S1C1	Q9s1c1 arabidopsis	380	60	13.0	195	2	Q6MQG8	Q6mqg8 bdellovibri
308	61	13.2	714	2	Q7RLU1	Q7rlu1 plasmodium	381	60	13.0	195	2	CAE78479	CAE78479 bdellovibri
309	61	13.2	790	1	LV14_YEAST	P40971 saccharomyc	382	60	13.0	308	2	Q74KR6	Q74kr6 lactobacill
310	61	13.2	827	2	Q9FMP8	Q9fmp8 arabidopsis	383	60	13.0	308	2	AA508503	AA508503 lactobaci
311	61	13.2	846	2	Q6JK79	Q6jk79 neodiprion	384	60	13.0	309	2	Q5YRC4	Q5yrc4 onion yello
312	61	13.2	1183	2	Q7NLE9	Q7nle9 gloeobacter	385	60	13.0	309	2	BAD04176	BAD04176 onion yel
313	61	13.2	1190	2	Q6CFF0	Q6cff0 yarrowia li	386	60	13.0	312	2	Q9UV78	Q9uv78 neisseria m
314	61	13.2	1312	2	Q8MVR0	Q8mvr0 dictyosteli	387	60	13.0	312	2	Q9K070	Q9k070 neisseria m
315	61	13.2	1774	1	MSAS_PENPA	P22367 penicillium	388	60	13.0	316	2	Q7RQS5	Q7rqs5 plasmodium
316	61	13.2	1805	2	Q7QVW0	Q7qvwo giardia lam	389	60	13.0	317	2	Q7R9W7	Q7r9w7 plasmodium
317	61	13.2	3365	2	Q6XHA7	Q6xha7 dictyosteli	390	60	13.0	356	2	Q8C3L4	Q8c3l4 yarrowia li
318	61	13.2	3365	2	AA083654	AA083654 dictyoste	391	60	13.0	358	2	Q8Y5A5	Q8y5a5 listeria mo
319	60.5	13.1	160	2	Q8DV24	Q8dv24 streptococc	392	60	13.0	358	2	Q71XK3	Q71xk3 listeria mo
320	60.5	13.1	171	2	Q8BYW3	Q8byw3 shigella fl	393	60	13.0	358	2	AA04962	AA04962 listeria
321	60.5	13.1	171	2	Q83J72	Q83j72 shigella fl	394	60	13.0	387	2	Q72QP2	Q72qp2 leptospira
322	60.5	13.1	174	2	Q6B7J3	Q6bj73 debaryomyce	395	60	13.0	387	2	Q8F5E9	Q8f5e9 leptospira
323	60.5	13.1	184	2	Q9XHW5	Q9xhw5 oryza sativ	396	60	13.0	387	2	Q8F5E9	Q8f5e9 leptospira

397	60	13.0	387	2	AAS70642	Aas70642 leptospir	470	59.5	12.9	598	2	Q7Q4T5	Q7q4t5 anopheles g
398	60	13.0	403	2	Q6P7X4	Q6p7x4 mus musculu	471	59.5	12.9	619	2	Q8A0A8	Q8a0a8 bacteroides
399	60	13.0	403	2	AAH61458	AAh61458 mus muscu	472	59.5	12.9	619	2	Q8A0A8	Q8a0a8 bacteroides
400	60	13.0	404	2	Q6BH39	Q6bh39 debaryomyce	473	59.5	12.9	652	2	Q6PYX3	Q6pyx3 rhizobium m
401	60	13.0	469	2	Q6W914	Q6w914 influenza a	474	59.5	12.9	652	2	Q6PYX3	Q6pyx3 rhizobium m
402	60	13.0	469	2	Q6W915	Q6w915 influenza a	475	59.5	12.9	663	2	AAS78464	Aas78464 brachydan
403	60	13.0	469	2	Q6W916	Q6w916 influenza a	476	59.5	12.9	663	2	AAS78464	Aas78464 brachydan
404	60	13.0	469	2	AAQ77410	AAq77410 influenza	477	59.5	12.9	792	2	Q6CXK1	Q6cxc1 kluyveromyc
405	60	13.0	469	2	AAQ77411	AAq77411 influenza	478	59.5	12.9	826	2	Q6SH33	Q6sh33 arabidopsis
406	60	13.0	469	2	AAQ77412	AAq77412 influenza	479	59.5	12.9	851	2	Q8V429	Q8v429 porcine cyt
407	60	13.0	486	2	Q22909	Q22909 arabidopsis	480	59.5	12.9	859	2	Q8V615	Q8v615 porcine cyt
408	60	13.0	502	2	Q6HBG7	Q6hbg7 bacillus th	481	59.5	12.9	860	2	Q8V430	Q8v430 porcine cyt
409	60	13.0	502	2	Q8ACB9	Q8acb9 human immun	482	59.5	12.9	860	2	Q8V613	Q8v613 porcine cyt
410	60	13.0	502	2	Q8ACB0	Q8acc0 human immun	483	59.5	12.9	861	2	Q6Y8U2	Q6y8u2 human immun
411	60	13.0	507	2	Q742D7	Q742d7 mycobacteri	484	59.5	12.9	861	2	Q8Q7G3	Q8q7g3 human immun
412	60	13.0	507	2	AAS03215	Aas03215 mycobacte	485	59.5	12.9	861	2	Q8Q7G3	Q8q7g3 human immun
413	60	13.0	514	2	Q9LQ20	Q9lq20 arabidopsis	486	59.5	12.9	885	2	CAE14697	CAe14697 leptospir
414	60	13.0	523	2	Q7WHS8	Q7whs8 bordetella	487	59.5	12.9	919	1	BCFI_MOUSE	Bcfi1697 leptospir
415	60	13.0	596	2	Q9VP62	Q9vp62 drosophila	488	59.5	12.9	949	2	Q9TT62	Q9tt62 hippodero
416	60	13.0	604	2	Q03944	Q03944 saccharomyc	489	59.5	12.9	961	2	Q86B19	Q86b19 dictyosteli
417	60	13.0	605	2	Q9SH28	Q9sh28 arabidopsis	490	59.5	12.9	1645	2	Q7TP73	Q7tp73 rattus norv
418	60	13.0	645	2	Q6CTH5	Q6cth5 kluyveromyc	491	59.5	12.9	1657	2	Q76NT8	Q76nt8 dictyosteli
419	60	13.0	653	1	RAB1_HUMAN	Rab1 human	492	59.5	12.9	1657	2	AAS38820	Aas38820 dictyoste
420	60	13.0	671	1	NCPR_MUSDO	Ncpr mus domest	493	59.5	12.9	1814	2	Q7PQL1	Q7pq11 anopheles g
421	60	13.0	687	2	Q9GYX9	Q9gyx9 armigeres s	494	59.5	12.9	2344	2	Q6QWJ0	Q6qwj0 rabbit hemo
422	60	13.0	697	2	Q7XJB9	Q7xjb9 oryza sativ	495	59.5	12.9	2344	2	Q9EMC2	Q9emc2 rabbit hemo
423	60	13.0	792	2	Q7RAU0	Q7rau0 plasmodium	496	59.5	12.9	2344	2	AAS13690	Aas13690 rabbit he
424	60	13.0	815	2	Q8BFX3	Q8bfx3 m mus muscu	497	59.5	12.8	82	2	Q97JV8	Q97jv8 clostridium
425	60	13.0	938	1	SYI_BUCAP	Syi bucap	498	59.5	12.8	102	2	P94587	P94587 clostridium
426	60	13.0	939	1	SYI_BUCHP	Syi buchp	499	59.5	12.8	158	2	Q8C8D9	Q8c8d9 mus musculu
427	60	13.0	962	1	SUUR_DROME	Suur drome	500	59.5	12.8	167	2	Q9WIB0	Q9wib0 beet wester
428	60	13.0	984	2	Q9GQX2	Q9gqx2 drosophila	501	59.5	12.8	192	2	Q9JF85	Q9jfb5 vaccinia vi
429	60	13.0	1028	2	Q74668	Q74668 pneumocysti	502	59.5	12.8	204	2	RUVA_PESM	Rufv34 pseudomonas
430	60	13.0	1039	2	Q8ZHA4	Q8zha4 yersinia pe	503	59.5	12.8	204	2	Q12097	Q12097 flammulina
431	60	13.0	1039	2	AAS63573	Aas63573 yersinia	504	59.5	12.8	208	2	Q82LK0	Q82lk0 streptomyc
432	60	13.0	1243	2	Q8JTP6	Q8jtp6 lumpy skin	505	59.5	12.8	214	2	Q73GF0	Q73gf0 wolbachia p
433	60	13.0	1279	2	Q86PE6	Q86pe6 drosophila	506	59.5	12.8	214	2	AAS14666	Aas14666 wolbachia
434	60	13.0	1365	2	Q7RRD5	Q7rrd5 plasmodium	507	59.5	12.8	241	2	Q8GEP4	Q8gep4 uncultured
435	60	13.0	1503	1	MRP6_HUMAN	Mrp6 human	508	59.5	12.8	241	2	Q74IR8	Q74ir8 lactobacill
436	60	13.0	1544	2	Q9WJF2	Q9wjf2 drosophila	509	59.5	12.8	261	1	EMCN_HUMAN	Eas09266 lactobaci
437	60	13.0	2868	2	Q86167	Q86167 dictyosteli	510	59.5	12.8	278	2	Q9KG03	Q9kg03 bacillus ha
438	60	13.0	3036	2	Q6G4Z7	Q6g4z7 bartonella	511	59.5	12.8	328	2	AA97571	AAb97571 caenorhab
439	60	13.0	3071	2	Q8QXL1	Q8qx1 sorghum mos	512	59.5	12.8	345	2	Q8EH11	Q8eh11 shewanella
440	60	13.0	3079	2	P89208	P89208 sorghum mos	513	59.5	12.8	362	2	Q6V5E8	Q6v5e8 capsella ru
441	59.5	12.9	77	2	Q6H458	Q6h458 oryza sativ	514	59.5	12.8	362	2	AA15469	AAr15469 capsella
442	59.5	12.9	158	2	Q6BD81	Q6bd81 macrobrachi	515	59.5	12.8	371	2	BAD20691	Bad20691 pseudomon
443	59.5	12.9	158	2	Q8I775	Q8it75 penaeus mon	516	59.5	12.8	375	1	GCDB_ACIFE	Gz2aa6 acidimono
444	59.5	12.9	187	1	Y467_VIBCH	Y467 vibrio chol	517	59.5	12.8	399	2	Q95G17	Q95g17 aristolochi
445	59.5	12.9	208	2	Q8EN96	Q8en96 oceanobacil	518	59.5	12.8	399	2	Q912D1	Q912d1 pseudomonas
446	59.5	12.9	245	2	Q7VIG5	Q7vig5 helicobacte	519	59.5	12.8	454	2	Q84L03	Q84l03 orchis lact
447	59.5	12.9	261	2	Q6TW12	Q6tw12 orf virus	520	59.5	12.8	469	2	Q6W911	Q6w911 influenza a
448	59.5	12.9	261	2	AA98183	AAr98183 orf virus	521	59.5	12.8	469	2	Q6W912	Q6w912 influenza a
449	59.5	12.9	264	2	Q8EX01	Q8ex01 mycoplasma	522	59.5	12.8	469	2	Q6W913	Q6w913 influenza a
450	59.5	12.9	280	2	Q8GC91	Q8gc91 clostridium	523	59.5	12.8	469	2	Q6W917	Q6w917 influenza a
451	59.5	12.9	307	2	Q73FE0	Q73fe0 bacillus ce	524	59.5	12.8	469	2	Q6W918	Q6w918 influenza a
452	59.5	12.9	307	2	AAS39002	Aas39002 bacillus	525	59.5	12.8	469	2	AAO77408	AAq77408 influenza
453	59.5	12.9	351	2	Q6MU19	Q6mu19 mycoplasma	526	59.5	12.8	469	2	AAO77409	AAq77409 influenza
454	59.5	12.9	351	2	CAE76867	CAe76867 mycoplas	527	59.5	12.8	469	2	AAQ77413	AAq77413 influenza
455	59.5	12.9	352	2	Q8A446	Q8a446 bacteroides	528	59.5	12.8	469	2	AAQ77414	AAq77414 influenza
456	59.5	12.9	373	2	Q84RF7	Q84rf7 arabidopsis	529	59.5	12.8	469	2	AAQ77415	AAq77415 influenza
457	59.5	12.9	374	2	Q9ZQA9	Q9zqa9 arabidopsis	530	59.5	12.8	474	2	Q28625	Q28625 oryctolagus
458	59.5	12.9	377	2	Q9LNF4	Q9lnf4 arabidopsis	531	59.5	12.8	498	2	Q995Q0	Q995q0 influenza a
459	59.5	12.9	378	2	Q8GXB3	Q8gxb3 arabidopsis	532	59.5	12.8	499	2	Q05518	Q05518 saccharomyc
460	59.5	12.9	467	2	Q8VUM4	Q8vum4 staphylococ	533	59.5	12.8	551	2	Q897S0	Q897s0 clostridium
461	59.5	12.9	544	2	Q6EZG6	Q6ezg6 caenorhabdi	534	59.5	12.8	584	2	Q897C9	Q897c9 clostridium
462	59.5	12.9	569	2	Q9W250	Q9w250 drosophila	535	59.5	12.8	641	1	SSX1_SOLTU	S9368 solanum tub
463	59.5	12.9	576	1	UN87_CAEEL	Un87 caeel	536	59.5	12.8	678	2	Q9VBV7	Q9vbv7 drosophila
464	59.5	12.9	579	2	Q80BA9	Q80ba9 rabbit hemo	537	59.5	12.8	708	1	MM09_RAT	P50282 rattus norv
465	59.5	12.9	579	2	Q8JZ14	Q8jz14 rabbit hemo	538	59.5	12.8	719	1	CL1D_BACTU	Q9x11 bacillus nor
466	59.5	12.9	579	2	Q9YND0	Q9ynd0 rabbit hemo	539	59.5	12.8	774	2	Q85G35	Q85g35 cyanidiosch
467	59.5	12.9	579	2	Q9YND4	Q9ynd4 rabbit hemo	540	59.5	12.8	793	1	YF06_MYCPN	P75280 mycoplasma
468	59.5	12.9	579	2	Q8UZ01	Q8uz01 rabbit hemo	541	59.5	12.8	803	2	Q7XKT7	Q7xkt7 oryza sativ
469	59.5	12.9	579	2	Q8UZ02	Q8uz02 rabbit hemo	542	59.5	12.8	813	2	Q6VIL7	Q6vil7 trypanosoma

543	59	12.8	813	2	AAQ56190	AaQ56190 trypanoso	616	58.5	12.7	652	2	Q25923	Q25923 plasmodium
544	59	12.8	871	2	O6LF60	O6lf60 plasmodium	617	58.5	12.7	706	2	Q26060	Q26060 pacifastacu
545	59	12.8	871	2	CAG25011	Cag25011 plasmodiu	618	58.5	12.7	738	2	Q7SD43	Q7sd43 neurospora
546	59	12.8	878	2	O87985	O87985 bordetella	619	58.5	12.7	754	2	Q8A120	Q8a120 pseudomonas
547	59	12.8	878	2	Q7W256	Q7w256 bordetella	620	58.5	12.7	856	2	Q9MB88	Q9mb88 brassica ol
548	59	12.8	878	2	Q7WR24	Q7wr24 bordetella	621	58.5	12.7	860	2	Q23916	Q23916 dictyosteli
549	59	12.8	939	2	O8HZS1	O8hzs1 myrmecophag	622	58.5	12.7	863	2	Q6BX88	Q6bx88 debaryomyce
550	59	12.8	945	2	O8HZS3	O8hzs3 tamandua te	623	58.5	12.7	869	2	Q6SG70	Q6sg70 uncultured
551	59	12.8	945	2	O9BDW1	O9bdw1 tamandua te	624	58.5	12.7	869	2	Q6UCX9	Q6ucx9 uncultured
552	59	12.8	958	2	Q7QFH3	Q7qfh3 anopheles g	625	58.5	12.7	869	2	AAR05261	Aar05261 unculture
553	59	12.8	960	2	Q8DSU4	Q8dsu4 vibrio vuln	626	58.5	12.7	869	2	AAR37992	Aar37992 unculture
554	59	12.8	970	1	DAB1_YEAST	P21657 saccharomyc	627	58.5	12.7	923	2	Q8T080	Q8t080 drosophila
555	59	12.8	970	1	PLK4_HUMAN	O00444 homo sapien	628	58.5	12.7	946	2	Q9EV24	Q9ev24 manheimia
556	59	12.8	1086	2	O6K3D4	O6k3d4 oryza sativ	629	58.5	12.7	953	1	LKA1_PASHA	P16535 pasteurella
557	59	12.8	1086	2	BAD22406	Bad22406 oryza sat	630	58.5	12.7	953	1	LKA3_PASHA	P51116 pasteurella
558	59	12.8	1089	2	O86KP4	O86kp4 dictyosteli	631	58.5	12.7	953	1	LKAB_PASHA	P51118 pasteurella
559	59	12.8	1116	1	MRH1_SCHPO	Q10407 schizosacch	632	58.5	12.7	953	2	Q6TB03	Q6tb03 manheimia
560	59	12.8	1128	2	O813W4	Q813w4 plasmodium	633	58.5	12.7	953	2	Q9ETG5	Q9etg5 pasteurella
561	59	12.8	1148	2	Q7S9L4	Q7s9l4 neurospora	634	58.5	12.7	953	2	Q9ETX2	Q9etx2 manheimia
562	59	12.8	1633	2	O8CMP4	O8cmp4 staphylococ	635	58.5	12.7	953	2	Q9EV23	Q9ev23 manheimia
563	59	12.8	1733	2	O9K1L4	Q9k1l4 staphylococ	636	58.5	12.7	953	2	Q9EV25	Q9ev25 manheimia
564	59	12.8	1804	2	Q9ZVU0	Q9zvv0 arabidopsis	637	58.5	12.7	953	2	Q9EV26	Q9ev26 manheimia
565	59	12.8	1893	2	Q9P9A8	Q9p9a8 uncultured	638	58.5	12.7	953	2	Q9EV27	Q9ev27 pasteurella
566	59	12.8	2259	2	Q921C2	Q921c2 mus musculu	639	58.5	12.7	953	2	Q9EV28	Q9ev28 pasteurella
567	59	12.8	2304	2	Q921C3	Q921c3 mus musculu	640	58.5	12.7	953	2	Q9EV29	Q9ev29 pasteurella
568	59	12.8	2607	2	Q7QP43	Q7qp43 giardia lam	641	58.5	12.7	953	2	Q9EV31	Q9ev31 pasteurella
569	59	12.8	2727	2	Q6NR00	Q6nr00 drosophila	642	58.5	12.7	953	2	Q9EV32	Q9ev32 pasteurella
570	59	12.8	2727	2	Q9VL06	Q9vl06 drosophila	643	58.5	12.7	953	2	Q9EV33	Q9ev33 pasteurella
571	59	12.8	2727	2	AAQ233602	AaQ233602 drosophil	644	58.5	12.7	953	2	Q9EV34	Q9ev34 pasteurella
572	58.5	12.7	71	2	O8LE92	Q8le92 arabidopsis	645	58.5	12.7	953	2	AAG40287	Aag40287 pasteurel
573	58.5	12.7	111	2	Q7PLG2	Q7plg2 drosophila	646	58.5	12.7	953	2	AAR09165	Aar09165 manheimi
574	58.5	12.7	155	2	O9KSQ7	Q9ksq7 vibrio chol	647	58.5	12.7	954	2	Q9EUE1	Q9eue1 pasteurella
575	58.5	12.7	187	1	YF29_VIBVU	O8acb0 vibrio vuln	648	58.5	12.7	955	1	LKAA_PASHA	P51117 pasteurella
576	58.5	12.7	187	1	Y869_VIBVY	Q7mhk0 vibrio vuln	649	58.5	12.7	955	2	Q9EUD4	Q9eud4 pasteurella
577	58.5	12.7	207	2	Q8BS65	Q8bs65 mus musculu	650	58.5	12.7	955	2	Q9EUD2	Q9eud2 pasteurella
578	58.5	12.7	223	2	Q92KD5	Q92kd5 helicobacte	651	58.5	12.7	1008	1	MOC4_CABEL	O45244 caenorhabdi
579	58.5	12.7	226	2	Q92KU4	Q92ku4 rhizobium m	652	58.5	12.7	1011	2	Q7XHN9	Q7xhn9 oryza sativ
580	58.5	12.7	234	2	O8RNN0	Q8rnn0 legionella	653	58.5	12.7	1011	2	BAC83208	Bac83208 oryza sat
581	58.5	12.7	264	2	O08643	O08643 mus musculu	654	58.5	12.7	1015	2	Q8BIW4	Q8biw4 mus musculu
582	58.5	12.7	268	2	Q79WF7	Q79wf7 streptococc	655	58.5	12.7	1136	2	Q615H9	Q615h9 oryza sativ
583	58.5	12.7	268	2	Q8KBE9	Q8kbe9 streptococc	656	58.5	12.7	1175	2	Q6BPD0	Q6bpd0 debaryomyce
584	58.5	12.7	268	2	Q8P277	Q8p277 streptococc	657	58.5	12.7	1177	2	Q9V414	Q9v414 drosophila
585	58.5	12.7	268	2	O9A156	Q9a156 streptococc	658	58.5	12.7	1333	2	Q9VUG6	Q9vug6 drosophila
586	58.5	12.7	371	2	Q7RUJ5	Q7ruj5 neurospora	659	58.5	12.7	1354	2	Q6VWH9	Q6vwh9 oryza sativ
587	58.5	12.7	373	2	Q9BH53	Q9bh53 rhizobium 1	660	58.5	12.7	1354	2	BAD16376	Bad16376 oryza sat
588	58.5	12.7	376	2	Q6BIH2	Q6bih2 debaryomyce	661	58.5	12.7	1467	2	Q7FDM5	Q7fdm5 plasmodium
589	58.5	12.7	383	2	Q9QB33	Q9qb33 human adeno	662	58.5	12.7	1553	2	Q6U629	Q6u629 brachydanio
590	58.5	12.7	387	2	Q8YJX4	Q8yjx4 anabaena sp	663	58.5	12.7	1553	2	AAQ84329	AaQ84329 brachydan
591	58.5	12.7	417	1	OXLIT_OXAFO	O51330 oxalobacter	664	58.5	12.7	1571	2	Q8S6M8	Q8s6m8 oryza sativ
592	58.5	12.7	439	1	QUIX_ACIAD	Q43923 acinetobact	665	58.5	12.7	1682	1	MSPI_PLAF3	P19598 plasmodium
593	58.5	12.7	440	2	Q6BU25	Q6bu25 debaryomyce	666	58.5	12.7	1688	2	Q764K9	Q764k9 plasmodium
594	58.5	12.7	456	2	Q93D60	Q93d60 escherichia	667	58.5	12.7	1688	2	Q764L0	Q764l0 plasmodium
595	58.5	12.7	463	2	Q9STL1	Q9stl1 drosophila	668	58.5	12.7	1688	2	BAD08401	Bad08401 plasmodiu
596	58.5	12.7	466	2	Q97K66	Q97k66 clostridium	669	58.5	12.7	1688	2	BAD08402	Bad08402 plasmodiu
597	58.5	12.7	480	2	Q6CPT6	Q6cpt6 kluyveromyc	670	58.5	12.7	1689	2	Q764K8	Q764k8 plasmodiu
598	58.5	12.7	490	2	Q753Y1	Q753y1 ashbya gos	671	58.5	12.7	1689	2	BAD08403	Bad08403 plasmodiu
599	58.5	12.7	490	2	AA553562	Q25615 onchocerca	672	58.5	12.7	1694	2	Q764L1	Q764l1 plasmodium
600	58.5	12.7	497	2	Q25615	Q25615 cryptospori	673	58.5	12.7	1694	2	Q9TZT5	Q9tzt5 plasmodium
601	58.5	12.7	507	2	Q86PQ7	Q86pq7 cryptospori	674	58.5	12.7	1694	2	Q9NHX1	Q9nhx1 plasmodium
602	58.5	12.7	515	2	Q6CK67	Q6ck67 kluyveromyc	675	58.5	12.7	1699	2	BAD08400	Bad08400 plasmodiu
603	58.5	12.7	531	1	SIG2_CANTR	Q12600 candida tro	676	58.5	12.7	1699	2	Q764L3	Q764l3 plasmodiu
604	58.5	12.7	532	2	Q9SKS1	Q9skel arabidopsis	677	58.5	12.7	1699	2	BAD08398	Bad08398 plasmodiu
605	58.5	12.7	542	1	THS_METJA	Q58405 methanococc	678	58.5	12.7	1700	2	Q764L2	Q764l2 plasmodiu
606	58.5	12.7	559	1	YFFI_SCHPO	Q94459 schizosacch	679	58.5	12.7	1700	2	BAD08399	Bad08399 plasmodiu
607	58.5	12.7	559	2	Q6P4K3	Q6p4k3 xenopus tro	680	58.5	12.7	1701	1	MSPI_PLAFF	P13819 plasmodium
608	58.5	12.7	559	2	AAH633364	Aah633364 xenopus t	681	58.5	12.7	1701	1	MSPI_PLAFM	P08569 plasmodium
609	58.5	12.7	561	2	Q9W8M1	Q9wm81 arabidopsis	682	58.5	12.7	1704	2	Q9TZT4	Q9tzt4 plasmodium
610	58.5	12.7	579	2	O8O953	O8o953 arabidopsis	683	58.5	12.7	1720	2	Q25922	Q25922 plasmodium
611	58.5	12.7	582	2	Q7Q5B0	Q7q5b0 anopheles g	684	58.5	12.7	1720	2	Q810U8	Q81ou8 plasmodium
612	58.5	12.7	602	2	Q7Q155	Q7q155 anopheles g	685	58.5	12.7	1726	1	MSPI_PLAPC	P04934 plasmodium
613	58.5	12.7	613	2	Q62372	Q62372 caenorhabdi	686	58.5	12.7	1726	1	MSPI_PLAPF	P50495 plasmodium
614	58.5	12.7	636	2	Q6XP25	Q6xp25 triticum ae	687	58.5	12.7	1757	2	Q7R137	Q7r137 giardia lam
615	58.5	12.7	636	2	AAP44536	Aap44536 triticum	688	58.5	12.7	3345	2	O46074	O46074 drosophila

689	58.5	12.7	3433	2	Q9W506	Q9W506 drosophila	762	58	12.6	1112	2	Q8BJ01	Q8bj01 mus musculus
690	58.5	12.7	3569	2	Q8IBV8	Q8ibv8 plasmodium	763	58	12.6	1196	2	Q6M580	Q6m580 corynebacte
691	58.5	12.7	6077	2	Q6LFH6	Q6lfh6 plasmodium	764	58	12.6	1196	2	CAF21515	CAF21515 corynebac
692	58.5	12.7	6077	2	CAG25332	CAG25332 plasmodiu	765	58	12.6	1217	2	Q7PNK0	Q7pnk0 anopheles g
693	58	12.6	110	2	Q6EQ82	Q6eq82 oryza sativ	766	58	12.6	1218	2	Q9V6T7	Q9v6t7 drosophila
694	58	12.6	191	2	Q8Q0L8	Q8q0l8 brachydanio	767	58	12.6	1221	2	Q8NQD1	Q8ngd1 corynebacte
695	58	12.6	193	2	Q835V0	Q835j0 enterococcu	768	58	12.6	1226	2	Q9SCZ2	Q9scz2 arabidopsis
696	58	12.6	201	2	Q8AV90	Q8ay90 brachydanio	769	58	12.6	1235	2	Q62244	Q62244 caenorhabdi
697	58	12.6	211	1	RS5_MYCGE	P47414 mycoplasma	770	58	12.6	1240	2	Q6BX13	Q6bx13 debaryomyce
698	58	12.6	225	2	Q6C5T3	Q6c5t3 yarrowia li	771	58	12.6	1252	2	Q6BVG6	Q6bv66 debaryomyce
699	58	12.6	248	1	TRYP_FUSOX	P35049 fusarium ox	772	58	12.6	1511	2	Q9I8E2	Q9i8e2 fugu rubrip
700	58	12.6	260	2	Q99WF8	Q99wf8 staphylococ	773	58	12.6	1607	2	Q7S408	Q7s408 neurospora
701	58	12.6	260	2	Q7A7F9	Q7a7f9 staphylococ	774	58	12.6	1607	2	CAF05854	CAF05854 neurospor
702	58	12.6	263	2	Q7SY54	Q7sy54 xenopus lae	775	58	12.6	1615	2	Q57415	Q57415 gallus gall
703	58	12.6	267	2	Q8DYF4	Q8dyf4 streptococc	776	58	12.6	1736	2	Q86AT9	Q86at9 dictyosteli
704	58	12.6	267	2	Q8E417	Q8e417 streptococc	777	58	12.6	1736	2	Q9SPH7	Q9sph7 dictyosteli
705	58	12.6	268	2	Q8IER7	Q8ier7 bacillus ce	778	58	12.6	1754	2	Q8RD81	Q8rd81 thermoaer
706	58	12.6	270	2	Q9I0T9	Q9i0t9 pseudomonas	779	58	12.6	1793	2	Q8EWM0	Q8ewm0 mycoplasma
707	58	12.6	288	2	Q50796	Q50796 borrelia bu	780	58	12.6	2287	2	Q6CT34	Q6ct34 kluyveromyc
708	58	12.6	288	2	Q50891	Q50891 borrelia bu	781	58	12.6	2392	2	Q8I0K1	Q8i0k1 caenorhabdi
709	58	12.6	292	2	Q02445	Q02445 helobdella	782	58	12.6	2407	2	Q7VSH5	Q7vsh5 caenorhabdi
710	58	12.6	324	2	Q912R0	Q912r0 dasheen mos	783	58	12.6	2592	2	Q19135	Q19135 caenorhabdi
711	58	12.6	336	2	Q6IIJ9	Q6ijj9 drosophila	784	58	12.6	2937	2	Q7N7K0	Q7n7k0 photorhabdu
712	58	12.6	348	2	Q8PTK5	Q8ptk5 methanosarc	785	58	12.6	3027	2	Q7MB03	Q7mb03 photorhabdu
713	58	12.6	351	2	Q96KA6	Q96ka6 homo sapien	786	58	12.6	3166	2	Q9W3Z0	Q9w3z0 drosophila
714	58	12.6	366	2	Q86VD3	Q86vd3 homo sapien	787	58	12.6	4872	2	Q7PMK5	Q7pmk5 anopheles g
715	58	12.6	368	2	Q72U87	Q72u87 leptospira	788	58	12.6	5108	2	Q7PJQ9	Q7pjq9 anopheles g
716	58	12.6	368	2	Q8F0U7	Q8f0u7 leptospira	789	58	12.6	5108	2	Q7FUR0	Q7fur0 anopheles g
717	58	12.6	368	2	AAS69391	Aas69391 leptospir	790	58	12.6	6420	2	P95814	P95814 streptomyc
718	58	12.6	425	2	Q8QB2	Q8qb2 pseudomonas	791	57.5	12.4	74	2	Q6H7K2	Q6h7k2 oryza sativ
719	58	12.6	427	1	ECTB MARHA	Q06060 marincoccu	792	57.5	12.4	113	2	Q7MEC5	Q7mec5 vibrio vuln
720	58	12.6	439	1	ACMA_LACIA	Q9cit4 lactococcus	793	57.5	12.4	119	2	Q8I2G0	Q8i2g0 plasmodium
721	58	12.6	455	1	POLG_WMV2T	Q89251 watermelon	794	57.5	12.4	141	2	Q9KSI4	Q9ks14 vibrio chol
722	58	12.6	455	2	Q9H0A4	Q9h0a4 homo sapien	795	57.5	12.4	143	2	Q6IGF1	Q6igf1 drosophila
723	58	12.6	483	2	Q9U0A1	Q9u0a1 homo sapien	796	57.5	12.4	154	2	Q6C662	Q6c662 yarrowia li
724	58	12.6	471	2	Q7U3Q1	Q7u3q1 synchococc	797	57.5	12.4	189	2	Q6D851	Q6d851 erwinia car
725	58	12.6	498	2	Q9EA34	Q9ea34 influenza a	798	57.5	12.4	195	2	Q8SJJ2	Q8sjj2 haemateria
726	58	12.6	503	2	Q8S6C0	Q8s6c0 oryza sativ	799	57.5	12.4	206	2	Q86FJ6	Q86fj6 schistosoma
727	58	12.6	520	2	Q7QM56	Q7qm56 anopheles g	800	57.5	12.4	233	2	Q7MIE4	Q7mie4 vibrio vuln
728	58	12.6	538	2	Q9FZH1	Q9fzh1 arabidopsis	801	57.5	12.4	241	2	Q6XKR7	Q6xkr7 triakis scy
729	58	12.6	563	2	Q6XND0	Q6xnd0 rhodococcus	802	57.5	12.4	241	2	AAP55511	AAP55511 triakis s
730	58	12.6	563	2	AAP73901	Aap73901 rhodococc	803	57.5	12.4	246	2	Q8DR01	Q8dr01 streptococc
731	58	12.6	599	2	Q9U3W0	Q9u3w0 drosophila	804	57.5	12.4	246	2	Q97SD2	Q97sd2 streptococc
732	58	12.6	599	2	Q9V680	Q9v680 drosophila	805	57.5	12.4	250	2	Q887H6	Q887h6 pseudomonas
733	58	12.6	605	2	Q801J8	Q801j8 salmo salar	806	57.5	12.4	256	2	Q6HC57	Q6hc57 bacillus th
734	58	12.6	619	2	Q81JL5	Q81jl5 plasmodium	807	57.5	12.4	263	2	Q89ZU7	Q89zu7 bacteroides
735	58	12.6	626	2	Q81GQ7	Q81gq7 drosophila	808	57.5	12.4	278	2	Q94BI7	Q94bi7 celosia sp.
736	58	12.6	642	2	Q9L423	Q9l423 anabaena sp	809	57.5	12.4	293	2	Q7MM50	Q7mm50 vibrio vuln
737	58	12.6	642	2	Q8YMW1	Q8ymw1 anabaena sp	810	57.5	12.4	308	2	Q84IF9	Q84if9 bacillus st
738	58	12.6	698	2	Q6G2K2	Q6g2k2 bartonella	811	57.5	12.4	312	2	Q9HEV2	Q9hev2 emericella
739	58	12.6	707	2	Q7NAN8	Q7nan8 mycoplasma	812	57.5	12.4	320	2	Q9HRV3	Q9hrv3 emericella
740	58	12.6	743	2	Q97KD9	Q97kd9 clostridium	813	57.5	12.4	329	1	PIP_ARATH	PIP_ARATH
741	58	12.6	762	2	Q9RM63	Q9rm63 xyloides od	814	57.5	12.4	329	2	Q94IB5	Q94ib5 arabidopsis
742	58	12.6	800	2	Q6NU13	Q6nu13 xenopus lae	815	57.5	12.4	342	2	Q24936	Q24936 eimeria ten
743	58	12.6	800	2	AAH68789	Aah68789 xenopus l	816	57.5	12.4	342	2	Q9UAR9	Q9uar9 eimeria ten
744	58	12.6	836	2	Q8YK11	Q8yk11 anabaena sp	817	57.5	12.4	342	2	Q9UAS1	Q9uas1 eimeria ten
745	58	12.6	902	2	Q8Q7H5	Q8q7h5 human immun	818	57.5	12.4	353	2	Q16478	Q16478 caenorhabdi
746	58	12.6	929	2	Q9BDT4	Q9bd4 corycteropus	819	57.5	12.4	365	2	Q9XZD8	Q9xzd8 tetrahymena
747	58	12.6	933	1	PERT_HUMAN	P07202 homo sapien	820	57.5	12.4	375	2	Q984T1	Q984t1 rhicobium l
748	58	12.6	938	2	Q9LERO	Q9ler0 arabidopsis	821	57.5	12.4	380	2	Q93Y05	Q93y05 arabidopsis
749	58	12.6	983	1	Y144_HUMAN	Q14157 homo sapien	822	57.5	12.4	391	2	Q6C783	Q6c783 yarrowia li
750	58	12.6	983	2	Q812D4	Q812d4 mus musculu	823	57.5	12.4	406	2	Q9GFZ6	Q9gft6 podolepis r
751	58	12.6	983	2	Q8BJ53	Q8bj53 mus musculu	824	57.5	12.4	406	2	Q9GG11	Q9gg11 podolepis a
752	58	12.6	989	2	Q6M0T9	Q6m0t9 methanococc	825	57.5	12.4	406	2	Q9GG12	Q9gg12 podolepis n
753	58	12.6	989	2	CAF29735	Caf29735 methanoco	826	57.5	12.4	407	2	Q7VYS2	Q7vys2 cryptospori
754	58	12.6	1004	2	Q6QXJ8	Q6qxj8 agrotis seg	827	57.5	12.4	412	2	Q08523	Q08523 ascaris suu
755	58	12.6	1004	2	AAS82683	Aas82683 agrototis s	828	57.5	12.4	412	2	Q08523	Q08523 ascaris suu
756	58	12.6	1014	2	Q8BIT6	Q8bit6 mus musculu	829	57.5	12.4	413	2	Q8SGS0	Q8sgs0 arabidopsis
757	58	12.6	1035	2	Q6FU56	Q6fu56 candida gla	830	57.5	12.4	425	2	Q8LFG1	Q8lfg1 arabidopsis
758	58	12.6	1035	2	Q812D5	Q812d5 mus musculu	831	57.5	12.4	436	2	Q35135	Q35135 neurospora
759	58	12.6	1067	2	Q8CIG7	Q8cig7 mus musculu	832	57.5	12.4	439	2	Q9A0Q8	Q9a0q8 emericella
760	58	12.6	1105	2	Q8K102	Q8k102 mus musculu	833	57.5	12.4	439	2	Q7TF25	Q7tf25 streptococc
761	58	12.6	1107	2	Q80X50	Q80x50 mus musculu	834	57.5	12.4	451	2	Q6LID0	Q6lid0 photobacter

835	57.5	12.4	451	2	CAG22950	Cag22950 photobact	908	57	12.3	158	2	Q8CYI0	Q8cyi0 streptococ
836	57.5	12.4	452	2	Q6G6P5	Q6g6p5 staphylococ	909	57	12.3	158	2	Q97PK5	Q97pk5 streptococ
837	57.5	12.4	452	2	Q8NV05	Q8nv05 staphylococ	910	57	12.3	186	1	Y304_HAEIN	P43980 haemophilus
838	57.5	12.4	452	2	Q99RK6	Q99rk6 staphylococ	911	57	12.3	198	2	Q95XP2	Q95xp2 caenorhabdi
839	57.5	12.4	452	2	Q7A3R8	Q7a3r8 staphylococ	912	57	12.3	216	2	Q844T6	Q844t6 uncultured
840	57.5	12.4	454	2	Q8D6W0	Q8d6w0 vibrio vuln	913	57	12.3	220	2	Q9AGL3	Q9agl3 arthrobacte
841	57.5	12.4	468	2	Q93436	Q93436 gallus gall	914	57	12.3	226	2	Q6LK99	Q6lk99 photobacter
842	57.5	12.4	469	2	Q6XV66	Q6xv66 influenza a	915	57	12.3	226	2	CAG22281	Cag22281 photobact
843	57.5	12.4	469	2	Q6XV67	Q6xv67 influenza a	916	57	12.3	247	1	M46D_MOUSE	Q99n07 mus musculu
844	57.5	12.4	469	2	AAO62023	AAo62023 influenza	917	57	12.3	266	2	Q8YQF9	Q8yqf9 anabaena sp
845	57.5	12.4	469	2	AAO62024	AAo62024 influenza	918	57	12.3	283	2	Q74FJ4	Q74fj4 geobacter s
846	57.5	12.4	475	2	Q9YU71	Q9yu71 drosophila	919	57	12.3	283	2	AAK33945	Aar33945 geobacter
847	57.5	12.4	491	1	FIBB_HUMAN	P02675 homo sapien	920	57	12.3	289	2	Q73RB1	Q73rel treponema d
848	57.5	12.4	501	2	Q6M0D0	Q6m0d0 methanococ	921	57	12.3	289	2	AAK10646	Aa10646 treponema
849	57.5	12.4	501	2	Q8YZT8	Q8yzt8 anabaena sp	922	57	12.3	302	2	Q97MM1	Q97mm1 clostridium
850	57.5	12.4	501	2	CAF29897	Ca29897 methanoco	923	57	12.3	307	2	Q7S2Z5	Q7s2z5 neurospora
851	57.5	12.4	510	2	Q97425	Q97425 drosophila	924	57	12.3	323	2	Q54343	Q54343 pasteurella
852	57.5	12.4	515	2	Q8G3W0	Q8g3w0 bifidobacte	925	57	12.3	323	2	Q54344	O54344 pasteurella
853	57.5	12.4	526	2	Q8R1B1	Q8r1b1 mus musculu	926	57	12.3	323	2	Q8YDY7	Q8ydy7 brucella me
854	57.5	12.4	528	2	Q6CGB3	Q6cgb3 yarowia li	927	57	12.3	325	2	Q72X47	Q72x47 bacillus ce
855	57.5	12.4	537	2	Q8LTF8	Q8lft8 oryza sativ	928	57	12.3	325	2	AA544431	Aa544431 bacillus
856	57.5	12.4	541	2	Q960X4	Q960x4 drosophila	929	57	12.3	327	2	Q8I306	Q8i3u6 bacillus ce
857	57.5	12.4	585	2	Q6YZP6	Q6yzp6 oryza sativ	930	57	12.3	372	2	Q93LM9	Q93lm9 cytophaga j
858	57.5	12.4	585	2	BAD01395	Bad01395 oryza sat	931	57	12.3	383	2	Q8FXK8	Q8fxk8 brucella su
859	57.5	12.4	585	2	BAD03738	Bad03738 oryza sat	932	57	12.3	395	2	Q835E5	Q83se5 enterococu
860	57.5	12.4	590	2	Q6P3Z4	Q6p3z4 mus musculu	933	57	12.3	404	2	Q95G26	Q95g26 aristolochi
861	57.5	12.4	590	2	Q8CCM5	Q8ccm5 mus musculu	934	57	12.3	414	2	Q46150	Q46150 paracentrot
862	57.5	12.4	590	2	AAH63757	Aah63757 mus muscu	935	57	12.3	423	2	Q7RB67	Q7rb67 plasmodium
863	57.5	12.4	594	1	ZF37_MOUSE	P17141 mus musculu	936	57	12.3	428	2	Q6J667	Q6j667 collimonas
864	57.5	12.4	594	2	Q8OYX7	Q8oyx7 mus musculu	937	57	12.3	440	2	Q72WM5	Q72wm5 bacillus ce
865	57.5	12.4	619	2	O24681	O24681 shigella bo	938	57	12.3	456	2	AA544513	Aa544513 bacillus
866	57.5	12.4	625	1	XYNA_PIRSP	I12667 shiomyces s	939	57	12.3	456	2	Q84L04	Q84l04 ophrys tent
867	57.5	12.4	637	2	Q72QV6	Q72qv6 leptospira	940	57	12.3	465	2	Q940C5	Q940c5 arabidopsis
868	57.5	12.4	637	2	Q8F4Z1	Q8f4z1 leptospira	941	57	12.3	469	2	Q6XV68	Q6xv68 influenza a
869	57.5	12.4	637	2	AA570578	Aa570578 leptospir	942	57	12.3	469	2	AAO62022	AAo62022 influenza
870	57.5	12.4	648	2	Q9U6B3	Q9u6b3 musca domes	943	57	12.3	472	2	Q6C063	Q6c063 yarowia li
871	57.5	12.4	651	2	Q25924	Q25924 plasmodium	944	57	12.3	478	2	Q6KZT2	Q6kzt2 microphilus
872	57.5	12.4	663	2	Q84TZ7	Q84tz7 oryza sativ	945	57	12.3	491	1	PYCA_METTH	O27939 methanobact
873	57.5	12.4	705	2	Q8H9R8	Q8h9r8 pseudomonas	946	57	12.3	506	2	P75996	Q79999 escherichia
874	57.5	12.4	731	2	Q8VH46	Q8vh46 rattus norv	947	57	12.3	539	2	Q9QP99	Q9qp99 daeheen mos
875	57.5	12.4	749	2	Q95ZB4	Q95zb4 leishmania	948	57	12.3	569	2	O28891	O28891 archaeoglob
876	57.5	12.4	751	1	VP4_ROTGI	P15155 rotavirus (949	57	12.3	569	2	Q8ZJQ9	Q8zjq9 yersinia pe
877	57.5	12.4	752	2	Q9C638	Q9c638 arabidopsis	950	57	12.3	583	2	Q9GUX6	Q9gux6 ciona savig
878	57.5	12.4	798	2	Q7WTT2	Q7wtt2 staphylococ	951	57	12.3	585	2	Q8CY67	Q8cy67 kluyveromyc
879	57.5	12.4	838	2	Q7XQU3	Q7xqu3 oryza sativ	952	57	12.3	613	2	Q8YKA1	Q8ykal sweet potat
880	57.5	12.4	854	1	LDRK_CRIGR	P35950 cricetulus	953	57	12.3	614	2	Q9UB07	Q9ub07 drosophila
881	57.5	12.4	869	2	Q7BKE7	Q7bke7 gamma-prote	954	57	12.3	614	2	Q9Y095	Q9y095 drosophila
882	57.5	12.4	869	2	Q9ZIX2	Q9zix2 pseudoaltr	955	57	12.3	614	2	Q7VKW0	Q7vkw0 haemophilus
883	57.5	12.4	869	2	AAQ62389	AAq62389 gamma-pro	956	57	12.3	645	2	Q6GA86	Q6ga86 staphylococ
884	57.5	12.4	878	2	Q8SQG6	Q8sgg6 nycteris gr	957	57	12.3	645	2	Q8NX66	Q8nx66 staphylococ
885	57.5	12.4	880	2	Q86KCO	Q86kc0 dictyosteli	958	57	12.3	645	2	Q9UXU5	Q9uxu5 staphylococ
886	57.5	12.4	926	2	Q86BWB	Q86bwb aplysia cal	959	57	12.3	645	2	Q7A656	Q7a656 staphylococ
887	57.5	12.4	930	2	Q7RHG3	Q7rhg3 plasmodium	960	57	12.3	654	2	Q93922	Q93922 pichia past
888	57.5	12.4	930	2	Q7VYG8	Q7v yg8 helicobacte	961	57	12.3	654	2	Q8QZ20	Q8qzz0 mus musculu
889	57.5	12.4	949	2	Q9FH15	Q9fh15 arabidopsis	962	57	12.3	686	2	Q8I553	Q8i553 plasmodium
890	57.5	12.4	968	2	Q7N650	Q7n650 photorhabdu	963	57	12.3	688	2	Q8I1E4	Q8i1e4 solanum tub
891	57.5	12.4	1024	2	Q8G9Z4	Q8g9z4 escherichia	964	57	12.3	704	1	LCRD_YEREN	P21210 yersinia en
892	57.5	12.4	1121	2	Q9M360	Q9m360 arabidopsis	965	57	12.3	706	2	Q7S7H9	Q7s7h9 neurospora
893	57.5	12.4	1227	2	Q7F2K3	Q7f2k3 fuscobacteri	966	57	12.3	706	2	Q87I12	Q87i12 neurospora
894	57.5	12.4	1607	2	Q6BJ03	Q6bj03 debaryomyce	967	57	12.3	747	2	Q8C4V1	Q8c4v1 mus musculu
895	57.5	12.4	1944	2	O94387	O94387 schizosacch	968	57	12.3	749	2	O59154	O59154 anaerocellu
896	57.5	12.4	2383	2	Q7O3H2	Q7q3h2 anopheles g	969	57	12.3	814	2	Q9M2W4	Q9m2w4 arabidopsis
897	57.5	12.4	2410	2	Q9YJW3	Q9y jw3 barley yell	970	57	12.3	834	2	Q8IC38	Q8ic38 bacillus ce
898	57.5	12.4	2566	2	Q8TSE7	Q8tse7 methanosarc	971	57	12.3	844	2	Q7XKTT9	Q7xtt9 oryza sativ
899	57.5	12.4	4037	2	Q74KU3	Q74ku3 lactobacill	972	57	12.3	844	2	Q9SC72	Q9sc72 oryza sativ
900	57.5	12.4	4037	2	AA508476	Aa508476 lactobaci	973	57	12.3	873	2	Q95X56	Q95x56 caenorhabdi
901	57.5	12.4	4654	2	Q8D418	Q8d418 vibrio vuln	974	57	12.3	891	2	O00101	O00101 phaeosphaer
902	57.5	12.4	4656	2	Q7MFI9	Q7mfi9 vibrio vuln	975	57	12.3	898	2	Q799Q8	Q799q8 escherichia
903	57	12.3	93	2	Q7M2H2	Q7m2h2 triakis scy	976	57	12.3	898	2	O28882	O28882 escherichia
904	57	12.3	110	2	Q6YQF3	Q6yqf3 onion yello	977	57	12.3	919	2	Q95X55	Q95x55 caenorhabdi
905	57	12.3	110	2	BAD04505	Bad04505 onion yel	978	57	12.3	949	2	O97306	O97306 plasmodium
906	57	12.3	145	2	Q7XHL2	Q7xhl2 oryza sativ	979	57	12.3	957	2	Q8QG06	Q8gg06 parus inorn
907	57	12.3	153	2	Q6IJ31	Q6ij31 drosophila	980	57	12.3	1070	2	Q8ZA36	Q8za36 yersinia pe

1127	56.5	12.2	1099	2	O68840	O68840 bacillus st	1200	56	12.1	232	2	O87CB5	O87cb5 xylella fas
1128	56.5	12.2	1107	2	O8PU06	Qpuc6 methanosarc	1201	56	12.1	236	2	O86XE6	Q86ke6 dictyosteli
1129	56.5	12.2	1137	2	Q3W6F6	Q9w6f6 gallus gall	1202	56	12.1	236	2	O9LIW6	Q9liw6 oryza sativ
1130	56.5	12.2	1147	2	Q7RF94	Q7rf94 plasmodium	1203	56	12.1	239	2	O6XIG7	Q6xig7 drosophila
1131	56.5	12.2	1167	2	O8W3A4	Q8w3a4 oryza sativ	1204	56	12.1	239	2	AAR09886	Aar09886 drosophil
1132	56.5	12.2	1221	2	Q7PMP6	Q7pmp6 anopheles g	1205	56	12.1	255	2	O94MX8	Q94mx8 haemophilus
1133	56.5	12.2	1248	2	O80TW8	Q80tw8 mus musculu	1206	56	12.1	269	2	O9VKV4	Q9vkv4 drosophila
1134	56.5	12.2	1304	2	O8IKW2	O8ikw2 plasmodium	1207	56	12.1	274	2	O88RQ5	O88rq5 pseudomonas
1135	56.5	12.2	1304	2	O8TI26	Q8ti26 dictyosteli	1208	56	12.1	275	2	O8NCL9	O8nc19 homo sapien
1136	56.5	12.2	1310	1	VAC3_HELPY	Q48253 helicobacte	1209	56	12.1	275	2	O8PAV8	O8pav8 xanthomonas
1137	56.5	12.2	1334	2	O6PGI7	Q6pgl7 mus musculu	1210	56	12.1	278	2	O8TEV0	Q8tev0 homo sapien
1138	56.5	12.2	1334	2	O8CAP0	Q8cap0 mus musculu	1211	56	12.1	279	2	O6TMU5	Q6tmu5 streptomyce
1139	56.5	12.2	1334	2	AAS56942	Aas56942 mus muscu	1212	56	12.1	279	2	O9RUP9	Q9rjp9 streptomyce
1140	56.5	12.2	1335	2	O7YI41	Q7y141 oryza sativ	1213	56	12.1	279	2	AAQ93528	Aa93528 streptomy
1141	56.5	12.2	1350	2	O7XHD8	Q7xhd8 oryza sativ	1214	56	12.1	282	2	O6LMN29	O6lmn29 photobacter
1142	56.5	12.2	1350	2	O7FWI2	Q7fw12 oryza sativ	1215	56	12.1	282	2	CAG21297	Cag21297 photobact
1143	56.5	12.2	1356	2	O8BTF8	Q8bt88 lactobacill	1216	56	12.1	287	2	O6GTX8	O6gtx8 homo sapien
1144	56.5	12.2	1406	2	O22411	Q22411 caenorhabdi	1217	56	12.1	292	1	YHH2_SCHPO	Y9usv4 schizosacch
1145	56.5	12.2	1428	1	TOP2_YEAST	P06786 saccharomyc	1218	56	12.1	305	1	RBSB_BACSU	P36949 bacillus su
1146	56.5	12.2	1428	2	O8TP86	Q8tf86 saccharomyc	1219	56	12.1	316	2	O9MUR1	Q9mur1 cavia porce
1147	56.5	12.2	1428	2	O8TG43	Q8tg43 saccharomyc	1220	56	12.1	323	2	O9Z7V9	Q9z7v9 chlamydia p
1148	56.5	12.2	1428	2	O8TG44	Q8tg44 saccharomyc	1221	56	12.1	327	2	O9GI64	O9gi64 paramachaer
1149	56.5	12.2	1428	2	O8TG46	Q8tg46 saccharomyc	1222	56	12.1	340	1	RFNG_XENLA	P79949 xenopus lae
1150	56.5	12.2	1428	2	O8TG47	Q8tg47 saccharomyc	1223	56	12.1	340	1	P79952	P79952 xenopus lae
1151	56.5	12.2	1428	2	O8TG53	Q8tg53 saccharomyc	1224	56	12.1	343	2	O7UP82	O7up82 rhodopirell
1152	56.5	12.2	1428	2	O8TG56	Q8tg56 saccharomyc	1225	56	12.1	350	2	O7QKY0	O7qky0 anopheles g
1153	56.5	12.2	1428	2	O8TG58	Q8tg58 saccharomyc	1226	56	12.1	353	2	O88E83	O88e83 pseudomonas
1154	56.5	12.2	1428	2	AA000518	Aa000518 saccharom	1227	56	12.1	362	1	ASG2_YEAST	P1163 saccharomyc
1155	56.5	12.2	1428	2	AA000530	Aa000530 saccharom	1228	56	12.1	362	2	O6QSK8	Q6qsk8 saccharomyc
1156	56.5	12.2	1428	2	AA000536	Aa000536 saccharom	1229	56	12.1	362	2	O6QSK9	Q6qsk9 saccharomyc
1157	56.5	12.2	1429	2	O90CH2	Q90ch2 human immun	1230	56	12.1	362	2	AAS56283	Aas56283 saccharom
1158	56.5	12.2	1436	2	O9VX60	Q9vx60 drosophila	1231	56	12.1	362	2	AAS56284	Aas56284 saccharom
1159	56.5	12.2	1459	2	Q7RLV6	Q7rlv6 giardia lam	1232	56	12.1	371	2	O50676	O50676 borrelia bu
1160	56.5	12.2	1509	2	O86B49	Q86b49 drosophila	1233	56	12.1	386	2	O7RLU5	O7rlu5 plasmodium
1161	56.5	12.2	1585	2	Q3F804	Q3f8q4 streptococc	1234	56	12.1	386	2	O9LJF9	Q9ljf9 arabidopsis
1162	56.5	12.2	1601	2	O8WSM1	Q8wsm1 caenorhabdi	1235	56	12.1	390	2	O9QZ56	Q9qzs6 mus musculu
1163	56.5	12.2	1680	2	O3UA02	Q3uaq2 caenorhabdi	1236	56	12.1	399	2	O94QA2	O94qa2 aristolochi
1164	56.5	12.2	2084	2	O8ILJ6	Q8ilj6 plasmodium	1237	56	12.1	399	2	O95G01	O95g01 aristolochi
1165	56.5	12.2	2146	2	O59897	Q59897 aspergillus	1238	56	12.1	399	2	O95G05	O95g05 aristolochi
1166	56.5	12.2	2146	2	O60026	O60026 aspergillus	1239	56	12.1	403	2	O74AS9	Q74as9 geobacter s
1167	56.5	12.2	2196	2	Q6DQW3	Q6dqw3 cercospora	1240	56	12.1	403	2	AA035648	Aar35648 geobacter
1168	56.5	12.2	3371	2	Q3J9C2	Q3j9c2 apoi virus.	1241	56	12.1	426	2	O9TXQ7	Q9txq7 caenorhabdi
1169	56.5	12.2	3416	2	O91B85	Q91b85 alkhurma vi	1242	56	12.1	428	2	O9PK87	O9pke7 chlamydia m
1170	56.5	12.2	3666	2	Q6UDX0	Q6udx0 plasmodium	1243	56	12.1	448	2	O9PKN2	O9pkn2 chlamydia m
1171	56.5	12.2	3666	2	AAQ73923	AaQ73923 plasmodiu	1244	56	12.1	456	2	O84KZ8	Q84kz8 anacampsis
1172	56.5	12.2	4392	2	O7ME58	Q7me58 vibrio vuln	1245	56	12.1	461	2	O6DN07	Q6dn07 streptococc
1173	56.5	12.2	4392	2	O9L4W3	Q9l4w3 streptomyce	1246	56	12.1	476	2	O6NSC1	Q6nsc1 homo sapien
1174	56	12.1	79	2	O9W312	Q9w312 drosophila	1247	56	12.1	476	2	O9ZNI4	Q9zni4 pseudomonas
1175	56	12.1	86	2	O38036	Q38036 human immun	1248	56	12.1	476	2	AAH70278	Aah70278 homo sapi
1176	56	12.1	86	2	O38037	Q38037 human immun	1249	56	12.1	478	2	O9H0J7	Q9h0j7 homo sapien
1177	56	12.1	86	2	O38039	Q38039 human immun	1250	56	12.1	503	2	O8UT08	Q8ut08 human immun
1178	56	12.1	113	2	O92R64	Q92r64 rhizobium m	1251	56	12.1	523	2	O93482	O93482 gallus gall
1179	56	12.1	114	2	O7WVF5	Q7wvf5 francisella	1252	56	12.1	525	1	MEPE_HUMAN	Q9nq76 homo sapien
1180	56	12.1	114	2	AA097847	Aa097847 francisel	1253	56	12.1	527	2	O8AXY3	Q8axy3 fugu rubrip
1181	56	12.1	131	2	O6LX75	Q6lx75 methanococc	1254	56	12.1	549	2	O9EW96	Q9ew96 streptomyce
1182	56	12.1	131	2	CAF31033	Caf31033 methanoco	1255	56	12.1	556	2	O22978	O22978 caenorhabdi
1183	56	12.1	153	1	ANF_RELCA	Q9gld0 felis silve	1256	56	12.1	562	2	O8BQZ7	Q8bqz7 mus musculu
1184	56	12.1	157	2	O9GTJ3	Q9gtj3 heterodera	1257	56	12.1	564	2	O8IL62	Q8il62 plasmodium
1185	56	12.1	158	2	O6FS38	Q6fs38 uncultured	1258	56	12.1	566	2	O8S551	Q8s551 cornus seri
1186	56	12.1	158	2	AA093820	Aa093820 unculture	1259	56	12.1	574	2	O6HBY4	Q6hby4 bacillus th
1187	56	12.1	160	2	O8YPR4	Q8ypa4 anabaena sp	1260	56	12.1	574	2	O72YG3	Q72yg3 bacillus ce
1188	56	12.1	175	2	O7RLK4	Q7rlk4 giardia lam	1261	56	12.1	574	2	O8LX57	Q8lxs7 bacillus an
1189	56	12.1	180	2	O6INM6	Q6ynm8 lactobacill	1262	56	12.1	574	2	AAS43959	Aas43959 bacillus
1190	56	12.1	180	2	AA138405	Aa138405 lactobaci	1263	56	12.1	574	2	AAT34282	Aat34282 bacillus
1191	56	12.1	187	2	O57224	O57224 vaccinia vi	1264	56	12.1	591	2	O6NTW7	Q6ntw7 xenopus lae
1192	56	12.1	187	2	AAT10521	Aat10521 vaccinia	1265	56	12.1	591	2	AAH68837	Aah68837 xenopus l
1193	56	12.1	192	1	VAL2_VACCC	P20989 vaccinia vi	1266	56	12.1	608	1	GHR_CHICK	Q02092 gallus gall
1194	56	12.1	192	2	Q6RZHI	Q6rzh1 rabbitpox v	1267	56	12.1	608	1	GLPO_STRPN	P35596 streptococc
1195	56	12.1	192	2	O8OHV7	Q8ohv7 vaccinia vi	1268	56	12.1	608	2	O6CRE2	Q6cre2 kluyveromyc
1196	56	12.1	192	2	AA049833	Aa049833 rabbitpox	1269	56	12.1	622	2	O7RVR5	Q7rv65 streptocora
1197	56	12.1	196	2	O9CH46	Q9ch46 lactococcus	1270	56	12.1	631	2	O9SR28	Q9sr28 arabidopsis
1198	56	12.1	205	2	O9NTC7	Q9ntc7 homo sapien	1271	56	12.1	704	1	MM09_CANFA	O18733 canis famil
1199	56	12.1	216	2	Q8GES0	Q8ges0 uncultured	1272	56	12.1	712	2	O19880	O19880 cyanidium c

1273	56	12.1	712	2	Q7CYV3	Q7CYV3 agrobacteri	1346	55.5	12.0	168	2	O22625	O22625 medicago sa
1274	56	12.1	712	2	Q8UEY1	Q8UEY1 agrobacteri	1347	55.5	12.0	169	2	O814F7	Q814F7 zephyranthe
1275	56	12.1	727	2	Q6CP99	Q6CP99 kluyveromyc	1348	55.5	12.0	174	2	O8DYT7	Q8DYT7 streptococc
1276	56	12.1	728	2	Q86JG1	Q86JG1 dictyosteli	1349	55.5	12.0	195	2	O8SJF3	Q8SJF3 heliobdella
1277	56	12.1	747	2	Q8BYH5	Q8BYH5 mus musculu	1350	55.5	12.0	207	2	Q7UMR2	Q7UMR2 rhodopirell
1278	56	12.1	763	2	Q7PR04	Q7PR04 anopheles g	1351	55.5	12.0	214	2	Q80BK2	Q80BK2 salinirine
1279	56	12.1	764	2	Q6MYH9	Q6MYH9 aspergillus	1352	55.5	12.0	217	1	GRE1_HUMAN	Q8Hav7 homo sapien
1280	56	12.1	764	2	CARF32024	Caf32024 aspergill	1353	55.5	12.0	217	1	AAP97195	Aap97195 homo sapi
1281	56	12.1	770	1	TPR1_CANFA	Q9Gld3 canis famil	1354	55.5	12.0	225	2	Q73ZN7	Q73zn7 mycobacteri
1282	56	12.1	793	2	Q6LF99	Q6LF99 plasmodium	1355	55.5	12.0	225	2	AAS03881	Aas03881 mycobacte
1283	56	12.1	793	2	CAG25027	Cag25027 plasmodiu	1356	55.5	12.0	252	2	Q7RFQW2	Q7rfqw2 plasmodium
1284	56	12.1	799	2	Q7S1A1	Q7S1A1 neurospora	1357	55.5	12.0	256	2	Q8PMK1	Q8pmk1 xanthomonas
1285	56	12.1	819	2	Q6K7Q5	Q6K7Q5 oryza sativ	1358	55.5	12.0	257	2	Q6PLA7	Q614a7 solanum dem
1286	56	12.1	850	1	PRSN_PIERA	Q9u8q4 pieris rapa	1359	55.5	12.0	257	2	AAT40498	Aat40498 solanum d
1287	56	12.1	870	2	O8A2I3	Q8a2i3 bacteroides	1360	55.5	12.0	283	2	Q97MH8	Q97mh8 clostridium
1288	56	12.1	874	2	Q6PDL7	Q6pdl7 mus musculu	1361	55.5	12.0	295	2	O76407	O76407 caenorhabdi
1289	56	12.1	874	2	AAS58637	Aas58637 mus muscu	1362	55.5	12.0	297	2	Q6CYV8	Q6cyv8 erwinia car
1290	56	12.1	883	2	Q6FCM2	Q6pdm2 mus musculu	1363	55.5	12.0	298	2	Q87BER6	Q87er6 xylella fas
1291	56	12.1	883	2	AAS59263	Aas59263 mus muscu	1364	55.5	12.0	298	2	Q9PGL2	Q9pgl2 xylella fas
1292	56	12.1	923	1	YELA_YEAST	P40017 saccharomyc	1365	55.5	12.0	300	2	Q94BQ5	Q94bq5 arabidopsis
1293	56	12.1	957	2	O8QG20	Q8gg20 meliphaga a	1366	55.5	12.0	306	1	MMGL_RAT	P49301 rattus norv
1294	56	12.1	960	2	O22214	O22214 arabidopsis	1367	55.5	12.0	307	2	Q723H2	Q723h2 homo sapien
1295	56	12.1	1012	2	Q9VP10	Q9vp10 drosophila	1368	55.5	12.0	308	2	Q91641	Q91641 pseudomonas
1296	56	12.1	1012	2	AAS1752	Aaf51752 drosophil	1369	55.5	12.0	321	1	MRGD_HUMAN	Q8tds7 homo sapien
1297	56	12.1	1032	2	Q73GM9	Q73gm9 wolbachia p	1370	55.5	12.0	321	2	AAR05120	Aar05120 homo sapi
1298	56	12.1	1032	2	AAS14587	Aas14587 wolbachia	1371	55.5	12.0	321	2	BAD20638	Bad20638 homo sapi
1299	56	12.1	1036	1	POL_HV2RO	P04584 human immun	1372	55.5	12.0	323	2	O6MM56	O6mm56 bdellovibri
1300	56	12.1	1061	2	O815M3	Q815m3 plasmodium	1373	55.5	12.0	323	2	CAE79849	Caet79849 bdellovib
1301	56	12.1	1077	2	Q8TE71	Q8te71 homo sapien	1374	55.5	12.0	334	2	Q6QHH7	Q6qhh7 staphylococ
1302	56	12.1	1108	2	Q8W4F7	Q8w4f7 arabidopsis	1375	55.5	12.0	334	2	AAS50176	Aas50176 staphyloc
1303	56	12.1	1110	2	Q8NIU9	Q8niu9 neurospora	1376	55.5	12.0	335	2	Q9ADL1	Q9adl1 polyangium
1304	56	12.1	1126	2	Q6IMN5	Q6imn5 homo sapien	1377	55.5	12.0	340	2	O81WR9	Q81wr9 homo sapien
1305	56	12.1	1127	1	Q6IMN6	Q6imn6 homo sapien	1378	55.5	12.0	351	2	O6VDN0	Q6vdn0 zea mays /m
1306	56	12.1	1138	1	PSD2_YEAST	P53037 saccharomyc	1379	55.5	12.0	351	2	AA011743	AA011743 zea mays
1307	56	12.1	1145	2	Q91KA7	Q91ka7 arabidopsis	1380	55.5	12.0	353	2	Q6MTU7	Q6mtu7 mycoplasma
1308	56	12.1	1184	2	O22725	O22725 arabidopsis	1381	55.5	12.0	353	2	CAE76939	Caet76939 mycoplaem
1309	56	12.1	1185	2	Q6BT72	Q6bt72 debaryomyce	1382	55.5	12.0	358	2	Q7R9N1	Q7r9n1 plasmodium
1310	56	12.1	1222	2	Q86HL6	Q86hl6 dictyosteli	1383	55.5	12.0	363	2	O8XHB7	Q8xb7 macaca fasc
1311	56	12.1	1222	2	Q86SA4	Q86sa4 dictyosteli	1384	55.5	12.0	364	2	O95KA0	Q95ka0 macaca fasc
1312	56	12.1	1394	1	HAP_HAEIN	P45387 haemophilus	1385	55.5	12.0	370	2	Q7CT78	Q7ct78 agrobacteri
1313	56	12.1	1419	2	O45092	O45092 caenorhabdi	1386	55.5	12.0	374	2	Q91645	Q9y645 homo sapien
1314	56	12.1	1522	2	Q6FL64	Q6fl64 candida gla	1387	55.5	12.0	399	2	Q9Y611	Q9y611 aristolochi
1315	56	12.1	1587	2	Q8WSH8	Q8wsh8 cryptospori	1388	55.5	12.0	399	2	Q95G13	Q95g13 aristolochi
1316	56	12.1	1687	2	Q61204	Q61204 mus musculu	1389	55.5	12.0	399	2	O95G15	Q95g15 aristolochi
1317	56	12.1	1770	2	O813A3	Q813a3 plasmodium	1390	55.5	12.0	406	2	O89GF2	Q89gf2 bradyrhizob
1318	56	12.1	1829	1	DPOL_THEST	Q33845 thermococcu	1391	55.5	12.0	425	2	O8XU25	Q8xu25 ralstonia s
1319	56	12.1	1861	2	Q6DFZ1	Q6dfz1 mus musculu	1392	55.5	12.0	426	2	Q7YU22	Q7yu22 drosophila
1320	56	12.1	1868	2	Q6H242	Q6h242 lactobacill	1393	55.5	12.0	436	1	RSMB_PSEPK	Q88rr3 pseudomonas
1321	56	12.1	2167	2	Q7RMJ1	Q7rmj1 plasmodium	1394	55.5	12.0	437	2	O44555	O44555 caenorhabdi
1322	56	12.1	2472	2	Q8MXN1	Q8mxn1 dictyosteli	1395	55.5	12.0	441	2	O8IUL5	Q8iul5 homo sapien
1323	56	12.1	2764	2	Q9WTS5	Q9wts5 mus musculu	1396	55.5	12.0	441	2	O96BR9	Q96br9 homo sapien
1324	56	12.1	2765	2	Q9R1K2	Q9rik2 rattus norv	1397	55.5	12.0	447	2	Q86BA6	Q86ba6 drosophila
1325	56	12.1	2910	2	Q81BY8	Q81by8 plasmodium	1398	55.5	12.0	449	2	Q82FC1	Q82fc1 streptomyc
1326	56	12.1	3191	2	Q912R2	Q912r2 daehee mos	1399	55.5	12.0	456	2	Q6BP79	Q6bp79 debaryomyce
1327	55.5	12.0	97	2	Q8MI83	Q8mi83 chaetospheae	1400	55.5	12.0	458	2	O8VN90	Q8vn90 helicobacte
1328	55.5	12.0	107	2	Q8H1A8	Q8hia8 hippeastrum	1401	55.5	12.0	458	2	O8VN91	Q8vn91 helicobacte
1329	55.5	12.0	109	2	Q6Y9V2	Q6y9v2 schizanthus	1402	55.5	12.0	462	2	O6RH31	Q6rh31 canis famil
1330	55.5	12.0	109	2	Q6Y9V3	Q6y9v3 schizanthus	1403	55.5	12.0	462	2	AAR97725	Aar97725 canis fam
1331	55.5	12.0	109	2	AA045733	Aa045733 schizanth	1404	55.5	12.0	463	2	Q85291	Q85291 potato mop-
1332	55.5	12.0	109	2	AA045734	Aa045734 schizanth	1405	55.5	12.0	463	2	Q91V54	Q91v54 potato mop-
1333	55.5	12.0	114	1	Y989_METUA	Q85396 methanococ	1406	55.5	12.0	466	2	Q6RH32	Q6rh32 canis famil
1334	55.5	12.0	120	2	Q99MW2	Q99mw2 mus musculu	1407	55.5	12.0	466	2	AAR97724	Aar97724 canis fam
1335	55.5	12.0	125	2	Q839P0	Q839p0 enterococcu	1408	55.5	12.0	469	2	Q6GYV9	Q6gyv9 influenza a
1336	55.5	12.0	125	2	Q839P0	Q839p0 enterococcu	1409	55.5	12.0	469	2	O8B197	O8b197 influenza a
1337	55.5	12.0	138	2	Q9FCE9	Q9fce9 streptomyc	1410	55.5	12.0	469	2	Q8B198	Q8b198 influenza a
1338	55.5	12.0	145	2	Q8H3B9	Q8h3b9 oryza sativ	1411	55.5	12.0	479	1	ETS2_CHICK	P10157 gallus gall
1339	55.5	12.0	148	2	Q53997	Q53997 salmonella	1412	55.5	12.0	485	2	Q93I71	Q93i71 escherichia
1340	55.5	12.0	152	2	Q8TG23	Q8tg23 yarrowia li	1413	55.5	12.0	487	2	Q9BV34	Q9bv34 homo sapien
1341	55.5	12.0	157	2	Q32650	Q32650 helicobacte	1414	55.5	12.0	493	2	Q9QBY8	Q9qby8 human immun
1342	55.5	12.0	157	2	Q32653	Q32653 helicobacte	1415	55.5	12.0	510	1	FKH_DROME	P14734 drosophila
1343	55.5	12.0	157	2	Q32655	Q32655 helicobacte	1416	55.5	12.0	544	2	O8FNV8	Q8fnv8 corynebacte
1344	55.5	12.0	158	2	Q79WS7	Q79ws7 streptococc	1417	55.5	12.0	550	2	Q8T4N7	Q8t4n7 caenorhabdi
1345	55.5	12.0	158	2	Q8K800	Q8k800 streptococc	1418	55.5	12.0	562	2	Q6BVE6	Q6bve6 debaryomyce
			159	2	Q8LK14	Q8lk14 zephyranthe							

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1419 55.5 12.0 580 2 Q7VC43 Q7vc43 prochloroco
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1422 55.5 12.0 585 2 Q8MQ17 Q8mq17 drosophila
1423 55.5 12.0 607 2 Q87Q57 Q87q57 vibrio para
1424 55.5 12.0 616 1 RFAL_HUMAN Rfal177 agrobacteri
1425 55.5 12.0 618 2 AAS94324 Aas94324 homo sapi
1426 55.5 12.0 628 2 Q9W572 Q9w572 drosophila
1427 55.5 12.0 630 2 Q6IHV0 Q6ihv0 drosophila
1428 55.5 12.0 633 2 Q6CEE4 Q6cee4 yarrowia li
1429 55.5 12.0 641 2 Q98UI4 Q98ui4 gallus gall
1430 55.5 12.0 657 2 Q72JH8 Q72jh8 thermus the
1431 55.5 12.0 657 2 AAS81140 Aas81140 thermus t
1432 55.5 12.0 685 2 Q7VDT2 Q7vdt2 prochloroco
1433 55.5 12.0 702 2 Q6BHB3 Q6bbh3 debaryomyce
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1435 55.5 12.0 710 2 Q6GV69 Q6gv69 oikopleura
1436 55.5 12.0 720 1 IF2_STARP IF2 STARP
1437 55.5 12.0 725 2 Q8GH18 Q8gh18 escherichia
1438 55.5 12.0 725 2 Q9Q119 Q9q119 escherichia
1439 55.5 12.0 725 2 Q93K73 Q93k73 escherichia
1440 55.5 12.0 725 2 Q8CY02 Q8cy02 escherichia
1441 55.5 12.0 725 2 Q8QRW1 Q8qrw1 chimpanzee
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1443 55.5 12.0 725 2 CAES5720 CAes5720 escherich
1444 55.5 12.0 731 2 Q80YS6 Q80ys6 mus musculu
1445 55.5 12.0 732 2 Q6ZPB4 Q6zpe4 mus musculu
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1447 55.5 12.0 749 2 Q9LE23 Q9le23 oryza sativ
1448 55.5 12.0 754 2 Q8UDAA Q8uda4 agrobacteri
1449 55.5 12.0 763 2 Q94EF8 Q94ef8 oryza sativ
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1451 55.5 12.0 766 1 TLK1_HUMAN Tlk1_HUMAN
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1453 55.5 12.0 768 2 Q7CKX9 Q7cxk9 agrobacteri
1454 55.5 12.0 770 2 Q6ZML2 Q6zml2 homo sapien
1455 55.5 12.0 770 2 BAD18713 Bad18713 homo sapi
1456 55.5 12.0 771 2 Q8IER0 Q8ier0 plasmodium
1457 55.5 12.0 786 2 Q77209 Q77209 trypanosoma
1458 55.5 12.0 805 2 Q7YTR3 Q7ytr3 cryptospori
1459 55.5 12.0 814 2 Q8S808 Q8s808 oryza sativ
1460 55.5 12.0 817 2 Q89928 Q89928 clostridium
1461 55.5 12.0 837 1 PHLD_MOUSE Phld_MOUSE
1462 55.5 12.0 839 1 PHLD_BOVIN Phld_BOVIN
1463 55.5 12.0 842 1 LPFC_SALTY Lpfc_SALTY
1464 55.5 12.0 843 2 Q84CNO Q84cno salmonella
1465 55.5 12.0 857 2 Q39392 Q39392 escherichia
1466 55.5 12.0 857 2 Q9SUVO Q9suvo arabidopsis
1467 55.5 12.0 866 2 Q9VHA6 Q9vha6 drosophila
1468 55.5 12.0 884 2 Q04085 Q04085 arabidopsis
1469 55.5 12.0 892 1 ATX7_HUMAN Atx7_HUMAN
1470 55.5 12.0 913 2 Q86B56 Q86b56 drosophila
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1472 55.5 12.0 915 2 Q8CVB9 Q8cvb9 kluyveromyc
1473 55.5 12.0 917 2 Q7RA65 Q7ra65 plasmodium
1474 55.5 12.0 918 2 Q8ER41 Q8er41 oceanobacil
1475 55.5 12.0 935 2 Q7NU34 Q7nu34 chronobacte
1476 55.5 12.0 955 2 Q04956 Q04956 cyanidium c
1477 55.5 12.0 958 2 Q89Z27 Q89zz7 bacteroides
1478 55.5 12.0 965 2 Q9SQH4 Q9sqh4 lilium long
1479 55.5 12.0 966 2 Q8QDU8 Q8qdj8 photorhabdu
1480 55.5 12.0 997 2 Q9FG03 Q9fg03 arabidopsis
1481 55.5 12.0 1030 2 Q01829 Q01829 pneumocysti
1482 55.5 12.0 1035 1 NANA_STRPN N2575 streptococc
1483 55.5 12.0 1035 1 NANA_STRR6 P62576 streptococc
1484 55.5 12.0 1053 2 Q757E0 Q757e0 ashbya goss
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1486 55.5 12.0 1122 2 Q8EW08 Q8ewd8 mycoplasma
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1488 55.5 12.0 1173 1 IF3X_SCHPO O59742 schizosacch
1489 55.5 12.0 1201 2 Q9VY99 Q9vy99 drosophila
1490 55.5 12.0 1292 2 Q20330 Q20330 caenorhabdi
1491 55.5 12.0 1317 2 Q96UG6 Q96ug6 gibberella

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1492 55.5 12.0 1323 2 Q7KSZ0 Q7ksz0 drosophila
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1494 55.5 12.0 1374 2 Q7YU77 Q7yu77 drosophila
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1496 55.5 12.0 1376 2 AAF54062 Aaf54062 drosophila
1497 55.5 12.0 1376 2 Q7CT17 Q7ct17 agrobacteri
1498 55.5 12.0 1520 2 Q8U9Q4 Q8u9q4 agrobacteri
1499 55.5 12.0 1520 2 Q8U9Q4 Q8u9q4 agrobacteri
1500 55.5 12.0 1593 1 AT12_HUMAN P58397 homo sapien
1501 55.5 12.0 1936 2 Q8I5A6 Q8i5a6 plasmodium

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ALIGNMENTS

RESULT 1

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Q6UWR2 Q6UWR2 PRELIMINARY; PRT; 90 AA.
ID Q6UWR2 PRELIMINARY; PRT; 90 AA.
AC Q6UWR2;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE CLECSF12.
GN ORFNames=UNQ589;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foeter J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Wagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL: AY358685; AAQ89048.1; -
SQ SEQUENCE 90 AA; 9840 MW; 6E4EFFD734264ACE CRC64;

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Query Match 100.0%; Score 462; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 6.le-42;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MTFPLSLLLLVCEAIWRNSGNTLENGYFLSRKNKHSHQPTOSLSDSVTPKAVKTT 60
Db 1 MTFPLSLLLLVCEAIWRNSGNTLENGYFLSRKNKHSHQPTOSLSDSVTPKAVKTT 60
Qy 61 GKGIKGRNLDRLGLILGAEGWGRGVKNT 90
Db 61 GKGIKGRNLDRLGLILGAEGWGRGVKNT 90

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RESULT 2

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AAQ89048 AAQ89048 PRELIMINARY; PRT; 90 AA.
ID AAQ89048 PRELIMINARY; PRT; 90 AA.
AC AAQ89048;
DT 02-MAR-2004 (TREMBLrel. 27, Created)
DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)
DE CLECSF12.
GN UNQ589.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

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RP SEQUENCE FROM N.A.
RX PubMed=12975309;
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heidens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wisand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
RT Effort to Identify Novel Human Secreted and Transmembrane Proteins: A
RT Bioinformatics Assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358685; AAQ8048.1; -.
SQ SEQUENCE 90 AA; 9840 MW; 6E4EFPD734264ACE CRC64;

Query Match 100.0%; Score 462; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 6.1e-42;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTFFLSLLLLLCEAIWRSNGSNTLENGYFLSRKNHNSQPTQSSLEDSVTPTKAVKT 60
Db |||||
QY 61 GKGIVKGRNLDRLGLILGAEAWGRGVKNT 90
Db |||||
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Db |||||

RESULT 3
Q96DR9 PRELIMINARY; PRT; 189 AA.
AC Q96DR9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Beta-glucan receptor isoform C.
GN Name=BGR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21570237; PubMed=11567029;
RA Willment J.A., Gordon S., Brown G.D.;
RT "Characterization of the human beta -glucan receptor and its
RT alternatively spliced isoforms.";
RL J. Biol. Chem. 276:43818-43823(2001).
DR EMBL; AF400597; AAL11713.1; -.
DR HSSP; O54709; 1HQ8.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0042287; P:MHC protein binding; NAS.
DR GO; GO:0008329; P:pattern recognition receptor activity; IDA.
DR GO; GO:0005529; P:sugar binding; IDA.
DR GO; GO:0019733; P:antibacterial humoral response (sensu Verte...; NAS.
DR GO; GO:0019734; P:antifungal humoral response (sensu Vertebrata); NAS.
DR GO; GO:0009756; P:carbohydrate mediated signaling; TAS.
DR GO; GO:0008037; P:cell recognition; IDA.
DR GO; GO:0042832; P:defense response to pathogenic protozoa; NAS.
DR GO; GO:0006910; P:phagocytosis, recognition; IDA.
DR GO; GO:0046803; P:reduction of virulence; NAS.
DR GO; GO:0042110; P:T-cell activation; TAS.
KW Receptor.
SQ SEQUENCE 189 AA; 21065 MW; F7DF9F76A4B6B59 CRC64;

Query Match 53.6%; Score 247.5; DB 2; Length 189;
Best Local Similarity 80.6%; Pred. No. 1.9e-18;
Matches 50; Conservative 4; Mismatches 3; Indels 5; Gaps 1;

RC TISSUE-Peripheral blood leukocyte;
RX MEDLINE=21570237; PubMed=11567029;
RA Willment J.A., Gordon S., Brown G.D.;
RT "Characterization of the human beta -glucan receptor and its
RT alternatively spliced isoforms.";
RL J. Biol. Chem. 276:43818-43823(2001).
DR EMBL; AF400597; AAL11713.1; -.
DR HSSP; O54709; 1HQ8.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0042287; P:MHC protein binding; NAS.
DR GO; GO:0008329; P:pattern recognition receptor activity; IDA.
DR GO; GO:0005529; P:sugar binding; IDA.
DR GO; GO:0019733; P:antibacterial humoral response (sensu Verte...; NAS.
DR GO; GO:0019734; P:antifungal humoral response (sensu Vertebrata); NAS.
DR GO; GO:0009756; P:carbohydrate mediated signaling; TAS.
DR GO; GO:0008037; P:cell recognition; IDA.
DR GO; GO:0042832; P:defense response to pathogenic protozoa; NAS.
DR GO; GO:0006910; P:phagocytosis, recognition; IDA.
DR GO; GO:0046803; P:reduction of virulence; NAS.
DR GO; GO:0042110; P:T-cell activation; TAS.
KW Receptor.
SQ SEQUENCE 189 AA; 21065 MW; F7DF9F76A4B6B59 CRC64;

Query Match 53.6%; Score 247.5; DB 2; Length 189;
Best Local Similarity 80.6%; Pred. No. 1.9e-18;
Matches 50; Conservative 4; Mismatches 3; Indels 5; Gaps 1;

QY 5 LSLILLVC-----EAIWRSNGSNTLENGYFLSRKNHNSQPTQSSLEDSVTPTKAVKT 59
Db |||||
QY 60 TG 61
Db |||
QY 113 TG 114

RESULT 5
Q96PA5 PRELIMINARY; PRT; 192 AA.
AC Q96PA5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Beta-glucan receptor isoform G.
GN Name=BGR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21570237; PubMed=11567029;
RA Willment J.A., Gordon S., Brown G.D.;
RT "Characterization of the human beta -glucan receptor and its
RT alternatively spliced isoforms.";
RL J. Biol. Chem. 276:43818-43823(2001).
DR EMBL; AF400601; AAL11717.1; -.
DR HSSP; O54709; 1HQ8.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0042287; P:MHC protein binding; NAS.
DR GO; GO:0008329; P:pattern recognition receptor activity; IDA.
DR GO; GO:0005529; P:sugar binding; IDA.
DR GO; GO:0019733; P:antibacterial humoral response (sensu Verte...; NAS.
DR GO; GO:0019734; P:antifungal humoral response (sensu Vertebrata); NAS.
DR GO; GO:0009756; P:carbohydrate mediated signaling; TAS.
DR GO; GO:0008037; P:cell recognition; IDA.
DR GO; GO:0042832; P:defense response to pathogenic protozoa; NAS.
DR GO; GO:0006910; P:phagocytosis, recognition; IDA.
DR GO; GO:0046803; P:reduction of virulence; NAS.
DR GO; GO:0042110; P:T-cell activation; TAS.
KW Receptor.
SQ SEQUENCE 192 AA; 21130 MW; 6F3350B1DFBEC921 CRC64;

Query Match 53.6%; Score 247.5; DB 2; Length 192;
Best Local Similarity 80.6%; Pred. No. 2e-18;
Matches 50; Conservative 4; Mismatches 3; Indels 5; Gaps 1;

QY 5 LSLILLVC-----EAIWRSNGSNTLENGYFLSRKNHNSQPTQSSLEDSVTPTKAVKT 59
Db |||||
QY 60 TG 61
Db |||
QY 113 TG 114

RESULT 5
Q96XN2 PRELIMINARY; PRT; 247 AA.
AC Q96XN2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Dendritic cell-associated C-type lectin-1 (DECTIN-1 receptor) (lectin-
DE like receptor 1) (Beta-glucan receptor isoform A).
GN Name=DECTIN-1; Synonyms=BGR, DECTIN1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;

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RN RP SEQUENCE FROM N.A.
RX MEDLINE=21363425; PubMed=11470510;
RA Yokota K., Takashima A., Bergstresser P.R., Ariizumi K.;
RT "Identification of a human homologue of the dendritic cell-associated
RT C-type lectin-1, dlectin-1.";
RL Gene 272:51-60(2001).
RN RP SEQUENCE FROM N.A.
RX Sobanov Y., Bernheiter A., Derdak S., Mechtcheriakova D., Duechler M.,
RA Kalthoff F., Hofer E.;
RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN RP SEQUENCE FROM N.A.
RX MEDLINE=21383615; PubMed=11491532;
RA Hernandez-Falcon P., Arce I., Roda-Navarro P., Fernandez-Ruiz E.;
RT "Cloning of human DECTIN-1, a novel C-type lectin-like receptor gene
RT expressed on dendritic cells.";
RL Immunogenetics 53:288-295(2001).
RN RP SEQUENCE FROM N.A.
RX Herranz-Falcon P., Arce I., Fernandez-Ruiz E.;
RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN RP SEQUENCE FROM N.A.
RX TISSUE=Peripheral blood leukocyte;
RX MEDLINE=21570237; PubMed=11567029;
RA Willment J.A., Gordon S., Brown G.D.;
RT "Characterization of the human beta -glucan receptor and its
RT alternatively spliced isoforms.";
RL J. Biol. Chem. 276:43818-43823(2001).
RN RP EMBL; AF313468; AAK37473.1; -.
DR EMBL; AJ312373; CAC43847.1; -.
DR EMBL; AY026769; AAK20114.2; -.
DR EMBL; AY400595; AAL11711.1; -.
DR HSSP; P26718; IKCG.
DR Genew; HGNC:1458; CLCSF12.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0042287; F:MHC protein binding; NAS.
DR GO; GO:0008329; F:pattern recognition receptor activity; IDA.
DR GO; GO:0005529; F:sugar binding; IDA.
DR GO; GO:0019733; P:antibacterial humoral response (sensu Verte...; NAS.
DR GO; GO:0019734; P:antifungal humoral response (sensu Vertebrata); NAS.
DR GO; GO:0009756; P:carbohydrate mediated signaling; TAS.
DR GO; GO:0008037; P:cell recognition; IDA.
DR GO; GO:0042832; P:phagocytosis, recognition; IDA.
DR GO; GO:0006910; P:defense response to pathogenic protozoa; NAS.
DR GO; GO:0046803; P:reduction of virulence; NAS.
DR GO; GO:0042110; P:T-cell activation; TAS.
DR InterPro; IPR002353; AntifreezeZell.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR PRINTS; PR00356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PSS0041; C_TYPE_LECTIN_2; 1.
DR Lectin; Receptor.
RW SEQUENCE 247 AA; 27627 MW; 98393E3697611B9 CRC64;
SQ
Query Match 53.6%; Score 247.5; DB 2; Length 247;
Best Local Similarity 80.6%; Pred. No. 2.6e-18;
Matches 50; Conservative 4; Mismatches 3; Indels 5; Gaps 1;
QY 5 LSLLLLLVC-----EAIWRNSGNTLENGYFLSRKNKHSQPTQSSLEDSVTPTKAVKT 59
DB 53 LCLVLIVAVLGTMAIWRNSGNTLENGYFLSRKNKHSQPTQSSLEDSVTPTKAVKT 112
QY 60 TG 61
DB 113 TG 114
RESULT 6
QBZR8
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ID QBZR8 PRELIMINARY; PRT; 247 AA.
AC QBZR8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Dendritic cell-associated C-type lectin-1.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22471764; PubMed=12406887;
RA Choi Y.K., Fallert B.A., Murphy-Corb M.A., Reinhart T.A.;
RT "Simian immunodeficiency virus dramatically alters expression of
RT homeostatic chemokines and dendritic cell markers during infection in
RT vivo.";
RL Blood 101:1684-1691(2003).
DR EMBL; AF508729; AAN47097.1; -.
DR HSSP; P22030; 1FVU.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro; IPR002353; AntifreezeZell.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR PRINTS; PR00356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PSS0041; C_TYPE_LECTIN_2; 1.
DR Lectin.
RW SEQUENCE 247 AA; 27648 MW; 9DF0D86DF2461518 CRC64;
SQ
Query Match 47.1%; Score 217.5; DB 2; Length 247;
Best Local Similarity 71.0%; Pred. No. 4.5e-15;
Matches 44; Conservative 6; Mismatches 7; Indels 5; Gaps 1;
QY 5 LSLLLLLVC-----EAIWRNSGNTLENGYFLSRKNKHSQPTQSSLEDSVTPTKAVKT 59
DB 53 LCLVLIVAVLGTMAIWRNSGNTLENGYFLSRKNKHSQPTQSSLEDSVTPTKAVKT 112
QY 60 TG 61
DB 113 TG 114
RESULT 7
QBZR8
ID QBZR8 PRELIMINARY; PRT; 244 AA.
AC QBZR8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Dectin-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21429420; PubMed=11544516;
RA Brown G.D., Gordon S.;
RT "Immune recognition. A new receptor for beta-glucans.";
RL Nature 413:36-37(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY534909; AAS37670.1; -.
DR GO; GO:0009897; C:external side of plasma membrane; IDA.
DR GO; GO:0001846; F:opsonin binding; IDA.
DR GO; GO:0001874; F:zymosan receptor activity; IDA.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu...; IDA.
DR GO; GO:0016337; P:cell-cell adhesion; IDA.
```

DR GO; GO:0001879; P:detection of yeast; IDA.
 DR GO; GO:0042535; P:positive regulation of tumor necrosis facto. . ; IDA.
 DR InterPro; IPR002353; AntifreezeII.

DR Pfam; PF00059; Lectin_C; 1.
 DR PRINTS; PR00356; ANTIFREEZEII.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00041; C TYPE LECTIN 2; 1.
 SQ SEQUENCE 244 AA; 27564 MW; DF84C12FF7592012 CRC64;

Query Match 31.1%; Score 143.5; DB 2; Length 244;
 Best Local Similarity 61.7%; Pred. No. 4.3e-07;
 Matches 29; Conservative 6; Mismatches 11; Indels 1; Gaps 1;

OY 15 AIWRNSGNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTG 61

Db 68 AFWRHSGRNPEKDSFLSRNKENH-KPTESLDEKVAFSPKASQTG 113

RESULT 8

ID Q9J150 PRELIMINARY; PRT; 244 AA.
 AC Q9J150;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE Dendritic cell-associated C-type lectin-1.
 GN Name=Clec5f12; Synonyms=Dectin-1;
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA1B/c;
 RX MEDLINE=20347934; PubMed=10779524;
 RA Arizumi K., Shen G.-L., Shikano S., Xu S., Ritter R. III,
 RA Kumamoto T., Edelbaum D., Morita A., Bergstresser P.R., Takashima A.;
 RT "Identification of a novel, dendritic cell-associated molecule,
 RT dectin-1, by subtractive cDNA cloning.";
 RL J. Biol. Chem. 275:20157-20167(2000).
 DR EMBL; AF262985; AAF72710.1; -.
 DR HSP; F22030; IFVU.
 DR MGD; MGI:1861431; Clec5f12.

DR GO; GO:0009897; C:external side of plasma membrane; IDA.
 DR GO; GO:0001846; F:opsonin binding; IDA.
 DR GO; GO:0001874; P:zymosan receptor activity; IDA.
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . ; IDA.
 DR GO; GO:0036337; P:cell-cell adhesion; IDA.
 DR GO; GO:0001879; P:detection of yeast; IDA.
 DR GO; GO:0042535; P:positive regulation of tumor necrosis facto. . ; IDA.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00059; Lectin_C; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00041; C TYPE LECTIN 2; 1.
 KW Lectin.

SQ SEQUENCE 244 AA; 27621 MW; 55A71C04E68CA002 CRC64;
 Query Match 31.1%; Score 143.5; DB 2; Length 244;
 Best Local Similarity 61.7%; Pred. No. 4.3e-07;
 Matches 29; Conservative 6; Mismatches 11; Indels 1; Gaps 1;

OY 15 AIWRNSGNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTG 61

Db 68 AFWRHSGRNPEKDSFLSRNKENH-KPTESLDEKVAFSPKASQTG 113

RESULT 9

AA037670 PRELIMINARY; PRT; 244 AA.
 ID AA037670;
 AC AA037670;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)

DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)

DE Dectin-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21429420; PubMed=11544516;
 RA Brown G.D., Gordon S.;

RT "Immune recognition. A new receptor for beta-glucans.";
 RL Nature 413:36-37(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Brown G.D. V., Gordon S.;

RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY534909; AAS37670.1; -.
 SQ SEQUENCE 244 AA; 27564 MW; DF84C12FF7592012 CRC64;

Query Match 31.1%; Score 143.5; DB 2; Length 244;
 Best Local Similarity 61.7%; Pred. No. 4.3e-07;
 Matches 29; Conservative 6; Mismatches 11; Indels 1; Gaps 1;

OY 15 AIWRNSGNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTG 61

Db 68 AFWRHSGRNPEKDSFLSRNKENH-KPTESLDEKVAFSPKASQTG 113

RESULT 10

ID Q8K1L4 PRELIMINARY; PRT; 244 AA.
 AC Q8K1L4;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Clec5f12 protein.

GN Name=Clec5f12;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=CZECH II;

RC TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;

RX MEDLINE=2388257; PubMed=12477932;

RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Souffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]
 RP SEQUENCE FROM N.A.

RC STRAIN=CZECH II;

RC TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;

RA Strausberg R.;

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC027742; AAH27742.1; -.

Q79XW8	PRELIMINARY;	PRT; 242 AA.
ID	AC	
05-JUL-2004	(TrEMBLrel. 27, Created)	
DT	DT	
05-JUL-2004	(TrEMBLrel. 27, Last sequence update)	
DT	DT	
05-JUL-2004	(TrEMBLrel. 27, Last annotation update)	
DE	Putative P1-type antirepressor (Phage associated).	
EE	OrderedLocusNames=SPS0602;	
OS	Streptococcus pyogenes (serotype M3).	
DS	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;	
OC	Streptococcus.	
OX	NCBI_TaxID=198466;	
XX	[1]	
RN	SEQUENCE FROM N.A.	
RRP	STRAIN=SSI-1;	
CRC	MEDLINE=22683278; PubMed=12799345;	
RXX	Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,	
RA	Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,	
RAA	Hayashi H., Hattori M., Hamada S.;	
RAA	"Genome sequence of an M3 strain of Streptococcus pyogenes reveals a	
RAA	large-scale genomic rearrangement in invasive strains and new insights	
RAA	into phage evolution.";	
RT	Genome Res. 13:1042-1055(2003).	
RL	EMBL; AP005143; BAC63697.1; -.	
DR	InterPro; IPR005039; Anti_rep.	
DRD	Pfam; PF03374; ANT; 1.	
DRD	SEQUENCE 242 AA; 27843 MW; 5AA85551447E366C CRC64;	
SQS		
Query Match 17.3%; Score 80; DB 2; Length 242;		
Best Local Similarity 35.9%; Pred. No. 3;		
Matches 23; Conservative 5; Mismatches 16; Indels 20; Gaps 3;		
QY	20 NSGSNTL-----ENGYPFLSRKNHNSOPTQSLSLE-----DSVTPTKAV-KT 59	
Ddb	163 NIGONKLFQWLNRANGYLISRRGESWNQPKSQMLGLFKLKTAINHSDGHTTTNVTPKV 222	
QY	60 TGKG 63	
Ddb	223 TGKG 226	
RESULT 13		
Q938N5	PRELIMINARY;	PRT; 242 AA.
IID	Q938N5	
AC	Q938N5;	
DT	01-DEC-2001 (TrEMBLrel. 19, Created)	
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)	
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	
DE	Antirepressor.	
OS	Temperate phage PhiNIH1.1.	
OC	Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.	
OX	NCBI_TaxID=173707;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Ikebe T., Wada A., Inagaki Y., Sugama K., Tanaka D., Suzuki R.,	
RA	Katsukawa C., Fujinaga Y., Abe Y., Watanabe H.,	
RA	The working group for Group A streptococci in Japan;	
RL	Submitted (OCT2005; AAL15047.1; -.	
DR	EMBL; AY050245; AAL15047.1; -.	
DR	GO; GO:0003677; F:DNA binding; IEA.	
DR	InterPro; IPR005039; Anti_rep.	
DR	Pfam; PF03374; ANT; 1.	
SQS	SEQUENCE 242 AA; 27843 MW; 5AA85551447E366C CRC64;	
Query Match 17.3%; Score 80; DB 2; Length 242;		
Best Local Similarity 35.9%; Pred. No. 3;		
Matches 23; Conservative 5; Mismatches 16; Indels 20; Gaps 3;		
QY	20 NSGSNTL-----ENGYPFLSRKNHNSOPTQSLSLE-----DSVTPTKAV-KT 59	
Ddb	163 NIGONKLFQWLNRANGYLISRRGESWNQPKSQMLGLFKLKTAINHSDGHTTTNVTPKV 222	
QY	60 TGKG 63	

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Db 223 TGKG 226

RESULT 14
O48391 PRELIMINARY; PRT; 238 AA.
AC O48391;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pl-antirepressor homolog
OS Streptococcus thermophilus bacteriophage TP-J34.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=73422;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=TP-J34;
RX MEDLINE=98122991; PubMed=9454717;
RA Neve H.; Zenz K.I.; Desiere F.; Koch A.; Heller K.J.; Brussow H.;
RT "Comparison of the lysogeny modules from the temperate Streptococcus
RT thermophilus bacteriophages TP-J34 and Sfi21: implications for the
RT modular theory of phage evolution.";
RL Virology 241:61-72(1998).
DR EMBL; AF020798; AAC03459.1; -.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR005039; Anti_rep.
DR Pfam; PF03374; ANT; 1.
SQ SEQUENCE 238 AA; 27081 MW; C30F3E97018EE651 CRC64;

Query Match 16.9%; Score 78; DB 2; Length 238;
Best Local Similarity 34.4%; Pred. No. 4.8;
Matches 22; Conservative 6; Mismatches 16; Indels 20; Gaps 3;

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Db 159 NIGQNKLFQWLSRNGYLSRRGDSWNQPTQKSMQLGLFELKKTININHADGHTTTNTTKV 218
QY 60 TGKG 63
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AC Q38585;
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DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Anti-repressor protein (Orf287 gp).
GN Name=orf287;
OS Streptococcus thermophilus bacteriophage Sfi21.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=64186;
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RC SEQUENCE FROM N.A.
RC MEDLINE=96204576; PubMed=8623559;
RA Bruttin A.; Desiere F.; Lucchini S.;
RT "Site-specific spontaneous deletions in three genome regions of a
RT temperate Streptococcus thermophilus phage.";
RL Virology 219:96-104(1996).
RN [2]
RC SEQUENCE FROM N.A.
RC MEDLINE=97344856; PubMed=9201223;
RA Bruttin A.; Desiere F.; Lucchini S.; Foley S.; Brussow H.;
RT "Characterization of the lysogeny module from the temperate
RT Streptococcus thermophilus bacteriophage Sfi21.";
RL Virology 233:136-148(1997).
RN [3]
RC SEQUENCE FROM N.A.
RA Brussow H.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
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RP SEQUENCE FROM N.A.
RA Desiere F.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RC SEQUENCE FROM N.A.
RX MEDLINE=98160788; PubMed=9499809;
RA Desiere F.; Lucchini S.; Brussow H.;
RT "Evolution of Streptococcus thermophilus bacteriophage genomes by
RT modular exchanges followed by point mutations and small deletions and
RT insertions.";
RL Virology 241:345-356(1998).
RN [6]
RC SEQUENCE FROM N.A.
RA Desiere F.; Lucchini S.; Bruttin A.; Brussow H.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; X95646; CAA64937.1; -.
DR EMBL; AF115103; AAD44100.1; -.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR005039; Anti_rep.
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Query Match 16.7%; Score 77; DB 2; Length 287;
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QY 60 TGKG 63
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Search completed: November 30, 2004, 14:44:00
Job time : 45 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 30, 2004, 14:43:16 ; Search time 22 Seconds
(without alignments)

271.301 Million cell updates/sec

Perfect score: 462

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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22	63.5	13.7	475	4	US-09-270-767-46709
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119	57.5	12.4	789	3	US-09-002-285-92	Sequence 92, Appl	192	56.5	12.2	789	4	US-10-099-285A-96	Sequence 96, Appl
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162	56.5	12.2	789	2	US-08-463-483A-32	Sequence 32, Appl	235	55.5	12.0	467	3	US-08-706-344C-28	Sequence 28, Appl
163	56.5	12.2	789	2	US-08-471-046A-29	Sequence 29, Appl	236	55.5	12.0	467	3	US-08-706-344C-30	Sequence 30, Appl
164	56.5	12.2	789	2	US-08-471-046A-32	Sequence 32, Appl	237	55.5	12.0	467	3	US-08-706-344C-32	Sequence 32, Appl
165	56.5	12.2	789	2	US-08-470-566B-29	Sequence 29, Appl	238	55.5	12.0	506	4	US-09-107-532A-5594	Sequence 5594, Ap
166	56.5	12.2	789	2	US-08-470-566B-32	Sequence 32, Appl	239	55.5	12.0	531	4	US-09-252-991A-22509	Sequence 22509, A
167	56.5	12.2	789	2	US-08-838-219B-2	Sequence 2, Appli	240	55.5	12.0	616	3	US-09-393-529-2	Sequence 2, Appli
168	56.5	12.2	789	2	US-08-838-219B-4	Sequence 4, Appli	241	55.5	12.0	616	4	US-09-396-149-7	Sequence 7, Appli
169	56.5	12.2	789	2	US-08-469-334-29	Sequence 29, Appl	242	55.5	12.0	689	4	US-09-425-335-2	Sequence 2, Appli
170	56.5	12.2	789	3	US-08-469-334-32	Sequence 32, Appl	243	55.5	12.0	720	4	US-09-710-279-2058	Sequence 2058, Ap
171	56.5	12.2	789	3	US-09-300-529-29	Sequence 29, Appl	244	55.5	12.0	720	4	US-09-668-113A-8	Sequence 8, Appli
172	56.5	12.2	789	3	US-09-300-529-32	Sequence 32, Appl	245	55.5	12.0	728	3	US-09-134-001C-4968	Sequence 4968, Ap
173	56.5	12.2	789	3	US-09-233-336A-4	Sequence 4, Appli	246	55.5	12.0	3241	4	US-09-841-786-1	Sequence 1, Appli
174	56.5	12.2	789	3	US-09-233-336A-4	Sequence 4, Appli	247	55	11.9	50	4	US-09-621-976-6173	Sequence 6173, Ap

248	55	11.9	50	4	US-09-621-976-6199	Sequence 6199, Ap	321	53.5	11.6	224	4	US-09-194-146-9	Sequence 9, Appli
249	55	11.9	60	4	US-09-248-796A-27675	Sequence 27675, A	322	53.5	11.6	252	4	US-09-602-787A-6	Sequence 6, Appli
250	55	11.9	157	3	US-08-718-130-4	Sequence 4, Appli	323	53.5	11.6	328	4	US-09-142-584-2	Sequence 2, Appli
251	55	11.9	158	4	US-09-248-796A-23151	Sequence 23151, A	324	53.5	11.6	328	4	US-09-142-584-4	Sequence 4, Appli
252	55	11.9	194	4	US-09-134-000C-6602	Sequence 6602, Ap	325	53.5	11.6	328	4	US-09-142-584-6	Sequence 6, Appli
253	55	11.9	278	4	US-09-134-000C-3724	Sequence 3724, Ap	326	53.5	11.6	368	1	US-08-303-238-3	Sequence 3, Appli
254	55	11.9	300	4	US-09-302-626B-182	Sequence 182, App	327	53.5	11.6	368	3	US-08-458-834-3	Sequence 3, Appli
255	55	11.9	345	4	US-09-248-796A-25189	Sequence 25189, A	328	53.5	11.6	368	6	5340934-2	Patent No. 5340934
256	55	11.9	347	4	US-09-710-279-462	Sequence 462, App	329	53.5	11.6	432	1	US-08-167-919A-11	Sequence 11, Appl
257	55	11.9	347	4	US-09-710-279-1268	Sequence 1268, Ap	330	53.5	11.6	432	3	US-08-715-106-11	Sequence 11, Appl
258	55	11.9	351	3	US-09-134-001C-5492	Sequence 5492, Ap	331	53.5	11.6	432	4	US-09-442-649-11	Sequence 11, Appl
259	55	11.9	418	4	US-09-252-991A-33098	Sequence 33098, A	332	53.5	11.6	432	4	US-09-543-681A-5369	Sequence 5369, Ap
260	55	11.9	490	4	US-09-252-991A-18155	Sequence 18155, A	333	53.5	11.6	450	3	US-09-518-657-4	Sequence 4, Appli
261	55	11.9	594	4	US-09-489-039A-13933	Sequence 13933, A	334	53.5	11.6	454	3	US-09-134-001C-3547	Sequence 3547, Ap
262	55	11.9	622	4	US-09-302-626B-185	Sequence 185, App	335	53.5	11.6	455	4	US-09-489-039A-14133	Sequence 14133, A
263	55	11.9	624	4	US-09-538-092-227	Sequence 227, App	336	53.5	11.6	565	4	US-09-270-767-41555	Sequence 41555, A
264	55	11.9	704	4	US-08-671-757A-11	Sequence 11, Appl	337	53.5	11.6	590	4	US-09-520-781-12	Sequence 12, Appl
265	55	11.9	1036	4	US-09-543-681A-7736	Sequence 7736, Ap	338	53.5	11.6	601	2	US-08-756-317-15	Sequence 15, Appl
266	55	11.9	1240	4	US-09-538-092-658	Sequence 658, App	339	53.5	11.6	609	4	US-09-396-149-6	Sequence 6, Appli
267	54.5	11.8	256	4	US-09-107-532A-4208	Sequence 4208, Ap	340	53.5	11.6	653	4	US-09-520-781-10	Sequence 10, Appl
268	54.5	11.8	299	4	US-09-270-767-61664	Sequence 61664, A	341	53.5	11.6	752	4	US-09-710-279-348	Sequence 348, App
269	54.5	11.8	309	4	US-09-248-796A-20897	Sequence 20897, A	342	53.5	11.6	804	3	US-09-134-001C-5218	Sequence 5218, Ap
270	54.5	11.8	328	4	US-09-964-850-4	Sequence 4, Appli	343	53.5	11.6	823	4	US-09-107-532A-5667	Sequence 5667, Ap
271	54.5	11.8	328	4	US-09-270-767-40048	Sequence 40048, A	344	53.5	11.6	1036	4	US-09-206-942-73	Sequence 73, Appl
272	54.5	11.8	347	4	US-09-270-767-55264	Sequence 55264, A	345	53.5	11.6	1477	1	US-08-302-832-4	Sequence 4, Appli
273	54.5	11.8	354	4	US-09-835-811-4	Sequence 811, A	346	53.5	11.6	1477	2	US-08-530-198-4	Sequence 4, Appli
274	54.5	11.8	354	4	US-09-248-796A-19107	Sequence 19107, A	347	53.5	11.6	1477	2	US-08-463-880-4	Sequence 4, Appli
275	54.5	11.8	405	4	US-08-823-516-145	Sequence 145, App	348	53.5	11.6	1477	2	US-08-728-470-4	Sequence 4, Appli
276	54.5	11.8	434	2	US-09-940-244-145	Sequence 145, App	349	53.5	11.6	1477	2	US-08-617-697-4	Sequence 4, Appli
277	54.5	11.8	434	4	US-09-270-767-43117	Sequence 43117, A	350	53.5	11.6	1477	2	US-08-719-641-4	Sequence 4, Appli
278	54.5	11.8	465	4	US-09-270-767-46109	Sequence 46109, A	351	53.5	11.6	1477	3	US-09-206-942-71	Sequence 71, Appl
279	54.5	11.8	509	4	US-09-461-325-144	Sequence 144, App	352	53.5	11.6	1477	4	US-08-276-852-80	Sequence 80, Appl
280	54.5	11.8	520	4	US-10-012-542-144	Sequence 144, App	353	53	11.5	122	1	US-08-899-575-80	Sequence 80, Appl
281	54.5	11.8	520	4	US-09-117-415B-2	Sequence 2, Appli	354	53	11.5	122	1	PCT-US95-08743-80	Sequence 80, Appl
282	54.5	11.8	520	4	US-09-117-415B-18	Sequence 18, Appl	355	53	11.5	122	5	US-09-270-767-59250	Sequence 59250, A
283	54.5	11.8	594	4	US-09-117-415B-22	Sequence 22, Appl	356	53	11.5	151	4	US-08-818-112-76	Sequence 76, Appl
284	54.5	11.8	613	4	US-09-117-415B-18	Sequence 18, Appl	357	53	11.5	151	4	US-09-072-967-76	Sequence 76, Appl
285	54.5	11.8	631	4	US-09-117-415B-20	Sequence 20, Appl	358	53	11.5	233	3	US-09-072-967-76	Sequence 76, Appl
286	54.5	11.8	631	4	US-09-117-415B-16	Sequence 16, Appl	359	53	11.5	233	3	US-09-072-967-76	Sequence 76, Appl
287	54.5	11.8	649	4	US-09-536-784-66	Sequence 66, Appl	360	53	11.5	233	3	US-09-072-967-76	Sequence 76, Appl
288	54.5	11.8	763	3	US-09-468-656A-10	Sequence 10, Appl	361	53	11.5	233	4	US-09-252-991A-21540	Sequence 21540, A
289	54.5	11.8	819	4	US-09-468-656A-4	Sequence 4, Appli	362	53	11.5	254	4	US-09-141-821-2	Sequence 2, Appli
290	54.5	11.8	838	4	US-09-583-110-5225	Sequence 5225, Ap	363	53	11.5	282	4	US-09-300-672-2	Sequence 2, Appli
291	54.5	11.8	838	4	US-09-538-092-87	Sequence 87, Appl	364	53	11.5	328	3	US-09-270-767-44084	Sequence 44084, A
292	54.5	11.8	2108	4	US-09-270-767-32529	Sequence 32529, A	365	53	11.5	341	4	US-07-966-187-12	Sequence 12, Appl
293	54.5	11.8	105	4	US-09-270-767-33121	Sequence 33121, A	366	53	11.5	370	1	US-07-966-187-14	Sequence 14, Appl
294	54	11.7	105	4	US-09-270-767-47746	Sequence 47746, A	367	53	11.5	370	1	US-07-966-187-18	Sequence 18, Appl
295	54	11.7	105	4	US-09-270-767-48338	Sequence 48338, A	368	53	11.5	370	1	US-09-252-991A-27724	Sequence 27724, A
296	54	11.7	105	4	US-09-107-532A-3479	Sequence 3479, Ap	369	53	11.5	433	4	US-09-212-609B-15	Sequence 15, Appl
297	54	11.7	133	4	US-09-134-000C-4294	Sequence 4294, Ap	370	53	11.5	488	3	US-09-248-796A-19639	Sequence 19639, A
298	54	11.7	143	4	US-09-540-236-3328	Sequence 3328, Ap	371	53	11.5	582	4	US-09-248-796A-15575	Sequence 15575, A
299	54	11.7	192	4	US-09-270-767-49100	Sequence 49100, A	372	53	11.5	593	4	US-09-014-897-2	Sequence 2, Appli
300	54	11.7	253	4	US-09-270-767-49100	Sequence 49100, A	373	53	11.5	731	1	US-08-731-716-2	Sequence 2, Appli
301	54	11.7	253	4	US-09-248-796A-27737	Sequence 27737, A	374	53	11.5	731	1	US-09-081-345-2	Sequence 2, Appli
302	54	11.7	298	4	US-09-248-796A-19462	Sequence 19462, A	375	53	11.5	807	3	US-09-483-039A-13531	Sequence 13531, A
303	54	11.7	304	4	US-09-543-681A-6123	Sequence 6123, Ap	376	53	11.5	852	4	US-09-206-942-61	Sequence 61, Appl
304	54	11.7	338	4	US-09-549-519-24	Sequence 11, Appl	377	53	11.5	915	4	US-09-206-942-59	Sequence 59, Appl
305	54	11.7	524	4	US-09-336-447A-11	Sequence 11, Appl	378	53	11.5	998	4	US-09-134-000C-3739	Sequence 3739, Ap
306	54	11.7	610	3	US-09-952-267B-11	Sequence 19, Appl	379	53	11.5	123	4	US-09-134-000C-3842	Sequence 3842, Ap
307	54	11.7	610	4	US-08-704-711A-19	Sequence 19, Appl	380	53	11.5	175	4	US-09-248-796A-26730	Sequence 26730, A
308	54	11.7	707	3	US-09-521-220-19	Sequence 20, Appl	381	53	11.5	175	4	US-08-044-621D-32	Sequence 32, Appl
309	54	11.7	707	3	US-09-391-104-20	Sequence 16, Appl	382	52.5	11.4	178	1	US-08-709-912-15	Sequence 15, Appl
310	54	11.7	707	3	US-08-448-489-16	Sequence 15, Appl	383	52.5	11.4	178	2	US-09-047-370-15	Sequence 15, Appl
311	54	11.7	708	3	US-09-328-352-5527	Sequence 81, Appl	384	52.5	11.4	186	4	US-09-673-763-12	Sequence 12, Appl
312	54	11.7	862	4	US-09-792-024-81	Sequence 32759, A	385	52.5	11.4	194	1	US-08-118-469A-7	Sequence 7, Appli
313	54	11.7	871	4	US-09-252-991A-32759	Sequence 15579, A	386	52.5	11.4	194	1	US-09-152-588-7	Sequence 7, Appli
314	54	11.7	922	4	US-09-248-796A-15579	Sequence 13574, A	387	52.5	11.4	200	4	US-09-107-532A-5968	Sequence 5968, Ap
315	54	11.7	977	4	US-09-489-039A-13574	Sequence 7376, Ap	388	52.5	11.4	216	4	US-09-270-767-44729	Sequence 44729, A
316	54	11.7	1138	4	US-09-543-681A-6179	Sequence 6179, Ap	389	52.5	11.4				
317	54	11.7	1148	4			390	52.5	11.4				
318	54	11.7	143	4			391	52.5	11.4				
319	53.5	11.6	162	4			392	52.5	11.4				
320	53.5	11.6					393	52.5	11.4				

394	52.5	11.4	263	2	US-08-685-992-5	Sequence 5, Appli	467	52.5	11.4	1493	4	US-09-538-092-1263	Sequence 1263, Ap
395	52.5	11.4	263	2	US-09-144-925-5	Sequence 5, Appli	468	52.5	11.4	1586	4	US-09-543-681A-5329	Sequence 5329, Ap
396	52.5	11.4	265	4	US-09-134-000C-6042	Sequence 6042, Ap	469	52	11.3	119	4	US-09-621-976-7661	Sequence 7661, Ap
397	52.5	11.4	297	4	US-09-270-767-34549	Sequence 34549, A	470	52	11.3	119	4	US-09-621-976-7662	Sequence 7662, Ap
398	52.5	11.4	297	4	US-09-270-767-49766	Sequence 49766, A	471	52	11.3	134	4	US-09-489-039A-9021	Sequence 9021, Ap
399	52.5	11.4	316	4	US-09-248-796A-14647	Sequence 14647, A	472	52	11.3	139	4	US-09-134-000C-5746	Sequence 5746, Ap
400	52.5	11.4	332	4	US-09-248-796A-21649	Sequence 21649, A	473	52	11.3	139	4	US-09-270-767-36667	Sequence 36667, A
401	52.5	11.4	348	4	US-09-270-767-42953	Sequence 42953, A	474	52	11.3	139	4	US-09-270-767-51884	Sequence 51884, A
402	52.5	11.4	354	4	US-09-823-153-8	Sequence 8, Appli	475	52	11.3	159	4	US-09-107-532A-6434	Sequence 6434, Ap
403	52.5	11.4	367	3	US-09-032-372-4	Sequence 4, Appli	476	52	11.3	161	4	US-10-101-464A-548	Sequence 548, App
404	52.5	11.4	382	4	US-09-328-352-4587	Sequence 4587, Ap	477	52	11.3	190	1	US-08-044-621D-26	Sequence 26, Appl
405	52.5	11.4	392	1	US-08-423-441-2	Sequence 2, Appli	478	52	11.3	190	1	US-08-044-621D-27	Sequence 27, Appl
406	52.5	11.4	407	2	US-08-875-972-4	Sequence 4, Appli	479	52	11.3	190	1	US-08-709-912-16	Sequence 16, Appl
407	52.5	11.4	432	4	US-09-778-510-2	Sequence 2, Appli	480	52	11.3	190	1	US-08-709-912-17	Sequence 17, Appl
408	52.5	11.4	439	4	US-09-248-796A-15955	Sequence 15955, A	481	52	11.3	190	2	US-09-047-370-16	Sequence 16, Appl
409	52.5	11.4	447	1	US-08-476-008-67	Sequence 67, Appl	482	52	11.3	190	2	US-09-047-370-17	Sequence 17, Appl
410	52.5	11.4	447	1	US-08-306-063-67	Sequence 67, Appl	483	52	11.3	190	4	US-09-570-856B-19	Sequence 19, Appl
411	52.5	11.4	447	1	US-08-833-485-67	Sequence 67, Appl	484	52	11.3	190	4	US-09-570-856B-22	Sequence 22, Appl
412	52.5	11.4	447	3	US-09-137-440-67	Sequence 67, Appl	485	52	11.3	208	4	US-08-956-171E-5200	Sequence 5200, Ap
413	52.5	11.4	449	4	US-09-355-214-3	Sequence 3, Appli	486	52	11.3	208	4	US-08-781-986A-5200	Sequence 5200, Ap
414	52.5	11.4	456	2	US-08-819-013-1	Sequence 1, Appli	487	52	11.3	218	4	US-09-134-000C-5097	Sequence 5097, Ap
415	52.5	11.4	456	4	US-09-355-214-1	Sequence 1, Appli	488	52	11.3	223	2	US-08-121-436A-2	Sequence 2, Appli
416	52.5	11.4	462	3	US-08-788-231A-15	Sequence 15, Appl	489	52	11.3	223	3	US-09-254-733-7	Sequence 7, Appli
417	52.5	11.4	463	2	US-08-670-479-18	Sequence 18, Appl	490	52	11.3	236	4	US-09-632-570-17	Sequence 17, Appl
418	52.5	11.4	463	3	US-08-670-964-4	Sequence 4, Appli	491	52	11.3	236	4	US-09-632-575-47	Sequence 47, Appl
419	52.5	11.4	463	3	US-08-888-077A-4	Sequence 4, Appli	492	52	11.3	238	4	US-09-252-991A-21314	Sequence 21314, A
420	52.5	11.4	463	4	US-08-937-834-6	Sequence 6, Appli	493	52	11.3	253	3	US-09-389-831-2	Sequence 2, Appli
421	52.5	11.4	463	4	US-09-895-035-12	Sequence 12, Appl	494	52	11.3	278	3	US-08-961-083-94	Sequence 94, Appl
422	52.5	11.4	465	4	US-09-496-239A-17	Sequence 17, Appl	495	52	11.3	278	4	US-09-536-784-94	Sequence 94, Appl
423	52.5	11.4	467	2	US-08-967-101-2	Sequence 2, Appli	496	52	11.3	278	4	US-09-248-796A-23487	Sequence 23487, A
424	52.5	11.4	467	2	US-08-967-101-134	Sequence 134, App	497	52	11.3	297	4	US-09-543-681A-8242	Sequence 8242, Ap
425	52.5	11.4	467	2	US-08-592-541-2	Sequence 2, Appli	498	52	11.3	305	4	US-09-710-279-2536	Sequence 2536, Ap
426	52.5	11.4	467	2	US-08-592-541-134	Sequence 134, App	499	52	11.3	309	4	US-09-724-623-72	Sequence 72, Appl
427	52.5	11.4	467	3	US-08-923-454A-10	Sequence 10, Appl	500	52	11.3	330	4	US-09-120-051D-47	Sequence 47, Appl
428	52.5	11.4	467	3	US-08-670-964-2	Sequence 2, Appli	501	52	11.3	336	4	US-09-107-532A-4289	Sequence 4289, Ap
429	52.5	11.4	467	3	US-08-888-077A-2	Sequence 2, Appli	502	52	11.3	373	4	US-10-140-002-388	Sequence 388, App
430	52.5	11.4	467	3	US-09-124-698-2	Sequence 2, Appli	503	52	11.3	410	4	US-09-270-767-44592	Sequence 44592, A
431	52.5	11.4	467	3	US-09-124-698-134	Sequence 134, App	504	52	11.3	450	4	US-09-489-039A-10052	Sequence 10052, A
432	52.5	11.4	467	3	US-09-127-480-2	Sequence 2, Appli	505	52	11.3	456	4	US-09-252-991A-11555	Sequence 11555, A
433	52.5	11.4	467	3	US-09-127-480-134	Sequence 134, App	506	52	11.3	468	4	US-09-248-796A-18502	Sequence 18502, A
434	52.5	11.4	467	3	US-08-496-841C-2	Sequence 2, Appli	507	52	11.3	477	4	US-09-248-796A-20553	Sequence 20553, A
435	52.5	11.4	467	3	US-08-496-841C-134	Sequence 134, App	508	52	11.3	506	4	US-09-248-796A-14859	Sequence 14859, A
436	52.5	11.4	467	3	US-08-832-867-3	Sequence 3, Appli	509	52	11.3	523	4	US-09-419-679B-14	Sequence 14, Appl
437	52.5	11.4	467	3	US-09-237-725A-1	Sequence 1, Appli	510	52	11.3	538	2	US-08-541-759B-2	Sequence 2, Appli
438	52.5	11.4	467	3	US-09-124-523-2	Sequence 2, Appli	511	52	11.3	543	4	US-09-543-681A-6901	Sequence 6901, Ap
439	52.5	11.4	467	3	US-09-124-523-134	Sequence 134, App	512	52	11.3	571	3	US-08-961-083-4	Sequence 4, Appli
440	52.5	11.4	467	3	US-09-375-318-3	Sequence 3, Appli	513	52	11.3	571	4	US-09-536-784-4	Sequence 4, Appli
441	52.5	11.4	467	4	US-09-636-796A-2	Sequence 2, Appli	514	52	11.3	645	3	US-09-328-501-1	Sequence 1, Appli
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443	52.5	11.4	467	4	US-08-431-048F-2	Sequence 2, Appli	516	52	11.3	650	3	US-09-232-200-79	Sequence 79, Appl
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743	50.5	10.9	1471	3	US-08-755-587-188	Sequence 188, App	816	50	10.8	567	3	US-08-311-703A-8	Sequence 8, Appli
744	50.5	10.9	2368	1	US-08-198-446B-15	Sequence 15, Appl	817	50	10.8	567	3	US-08-446-936B-8	Sequence 8, Appli
745	50.5	10.9	2368	2	US-08-870-693-15	Sequence 15, Appl	818	50	10.8	567	3	US-09-183-543-8	Sequence 8, Appli
746	50.5	10.9	2781	4	US-09-698-295-10	Sequence 10, Appl	819	50	10.8	567	3	US-08-446-936A-8	Sequence 8, Appli
747	50.5	10.9	2907	3	US-09-698-295-1	Sequence 1, Appli	820	50	10.8	567	3	US-09-239-864A-11	Sequence 11, Appl
748	50.5	10.9	3169	3	US-09-453-702B-257	Sequence 257, App	821	50	10.8	567	4	US-09-878-905-11	Sequence 11, Appl
749	50	10.8	29	1	US-08-520-599-3	Sequence 3, Appli	822	50	10.8	567	4	US-09-267-963D-36	Sequence 36, Appl
750	50	10.8	33	1	US-08-520-599-2	Sequence 2, Appli	823	50	10.8	567	5	PCT-US92-09326-4	Sequence 4, Appli
751	50	10.8	42	1	US-08-520-599-1	Sequence 1, Appli	824	50	10.8	568	4	US-09-328-352-5460	Sequence 5460, App
752	50	10.8	43	2	US-08-483-926A-3	Sequence 3, Appli	825	50	10.8	573	1	US-08-200-512-2	Sequence 2, Appli
753	50	10.8	43	2	US-08-854-768-3	Sequence 3, Appli	826	50	10.8	584	3	US-09-102-528-12	Sequence 12, Appl
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755	50	10.8	74	4	US-09-621-976-4946	Sequence 4946, App	828	50	10.8	623	4	US-09-252-991A-31173	Sequence 31173, A
756	50	10.8	146	4	US-09-270-767-36607	Sequence 36607, App	829	50	10.8	627	4	US-09-071-035-218	Sequence 218, App
757	50	10.8	146	4	US-09-270-767-51824	Sequence 51824, A	830	50	10.8	659	4	US-09-134-000C-6124	Sequence 6124, App
758	50	10.8	174	4	US-09-248-796A-15628	Sequence 15628, A	831	50	10.8	660	4	US-09-273-163-6	Sequence 6, Appli
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833	50	10.8	715	4	US-09-462-917A-134	Sequence 134, App	906	49.5	10.7	382	4	US-09-270-767-45026	Sequence 45026, A
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835	50	10.8	788	4	US-09-538-092-567	Sequence 567, App	908	49.5	10.7	392	4	US-09-540-236-1947	Sequence 1947, App
836	50	10.8	817	4	US-09-489-039A-8184	Sequence 8184, App	909	49.5	10.7	392	4	US-09-540-236-1947	Sequence 2045, A
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838	50	10.8	831	4	US-09-736-457-1819	Sequence 1819, App	911	49.5	10.7	405	4	US-09-328-352-6717	Sequence 6717, App
839	50	10.8	831	4	US-09-671-325-1819	Sequence 1819, App	912	49.5	10.7	415	4	US-09-489-039A-8402	Sequence 8402, App
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841	50	10.8	941	3	US-09-952-267B-9	Sequence 9, Appli	914	49.5	10.7	541	4	US-09-538-092-347	Sequence 347, App
842	50	10.8	1010	3	US-09-134-001C-5178	Sequence 5178, App	915	49.5	10.7	541	4	US-09-489-039A-8233	Sequence 8233, App
843	50	10.8	1028	4	US-09-543-681A-7181	Sequence 7181, App	916	49.5	10.7	552	4	US-09-248-796A-23118	Sequence 23118, A
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845	50	10.8	1146	4	US-09-824-734-2	Sequence 2, Appli	918	49.5	10.7	567	4	US-09-489-039A-12032	Sequence 12032, A
846	50	10.8	1281	4	US-09-489-039A-10396	Sequence 10396, A	919	49.5	10.7	583	4	US-09-543-681A-5823	Sequence 5823, App
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851	50	10.8	1867	3	US-09-134-916A-5	Sequence 5, Appli	924	49.5	10.7	636	4	US-09-270-767-45245	Sequence 45245, A
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858	49.5	10.7	119	4	US-09-513-999C-6184	Sequence 6184, App	931	49.5	10.7	884	4	US-09-841-786-3	Sequence 3, Appli
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862	49.5	10.7	135	4	US-09-252-991A-26097	Sequence 26097, A	935	49.5	10.7	1091	3	US-09-327-536-2	Sequence 2, Appli
863	49.5	10.7	149	4	US-09-270-767-45884	Sequence 45884, A	936	49.5	10.7	1161	3	US-09-098-707A-2	Sequence 2, Appli
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866	49.5	10.7	157	3	US-08-815-927-4	Sequence 4, Appli	939	49.5	10.7	1442	1	US-08-013-986A-3	Sequence 3, Appli
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868	49.5	10.7	157	3	US-09-435-242-4	Sequence 4, Appli	941	49.5	10.7	1589	4	US-09-543-681A-4998	Sequence 4998, App
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870	49.5	10.7	170	2	US-08-327-357A-1	Sequence 1, Appli	943	49.5	10.7	1702	3	US-09-839-996-5	Sequence 5, Appli
871	49.5	10.7	170	3	US-09-007-520-1	Sequence 1, Appli	944	49.5	10.7	1702	4	US-10-080-505-5	Sequence 5, Appli
872	49.5	10.7	170	3	US-09-055-263-1	Sequence 1, Appli	945	49.5	10.7	1702	5	PCT-US95-10661A-5	Sequence 5, Appli
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874	49.5	10.7	170	3	US-08-342-408B-2	Sequence 2, Appli	947	49	10.6	65	4	US-09-248-796A-27358	Sequence 27358, A
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876	49.5	10.7	171	3	US-09-137-759-2	Sequence 2, Appli	949	49	10.6	95	3	US-08-789-333F-46	Sequence 46, Appli
877	49.5	10.7	171	3	US-08-953-937-2	Sequence 2, Appli	950	49	10.6	95	4	US-08-787-738B-46	Sequence 46, Appli
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881	49.5	10.7	187	4	US-08-635-886C-209	Sequence 209, App	954	49	10.6	155	4	US-09-328-352-5061	Sequence 5061, App
882	49.5	10.7	187	4	US-08-974-690C-209	Sequence 209, App	955	49	10.6	159	2	US-08-271-397-1	Sequence 1, Appli
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884	49.5	10.7	197	4	US-09-512-563C-54	Sequence 54, Appli	957	49	10.6	159	5	PCT-US91-07280-1	Sequence 1, Appli
885	49.5	10.7	201	4	US-09-252-991A-21340	Sequence 21340, A	958	49	10.6	161	4	US-09-540-236-3245	Sequence 3245, App
886	49.5	10.7	205	4	US-09-248-796A-15224	Sequence 15224, A	959	49	10.6	163	1	US-08-256-261-17	Sequence 17, Appli
887	49.5	10.7	209	4	US-09-248-796A-18808	Sequence 18808, A	960	49	10.6	163	3	US-08-852-299-17	Sequence 17, Appli
888	49.5	10.7	235	4	US-09-252-991A-22275	Sequence 22275, A	961	49	10.6	167	4	US-08-468-996-7	Sequence 7, Appli
889	49.5	10.7	239	4	US-09-248-796A-25501	Sequence 25501, A	962	49	10.6	173	4	US-09-270-767-60931	Sequence 60931, A
890	49.5	10.7	258	4	US-09-248-796A-16045	Sequence 16045, A	963	49	10.6	176	4	US-09-328-352-7007	Sequence 7007, App
891	49.5	10.7	267	3	US-08-557-128-4	Sequence 4, Appli	964	49	10.6	179	4	US-09-248-796A-17828	Sequence 17828, A
892	49.5	10.7	267	3	US-09-242-690A-36	Sequence 36, Appli	965	49	10.6	193	4	US-08-635-886C-223	Sequence 223, App
893	49.5	10.7	267	4	US-09-908-855-36	Sequence 36, Appli	966	49	10.6	193	4	US-08-974-690C-223	Sequence 223, App
894	49.5	10.7	267	4	US-09-270-767-60513	Sequence 60513, A	967	49	10.6	193	4	US-09-878-281A-180	Sequence 180, App
895	49.5	10.7	330	4	US-09-614-912-122	Sequence 122, App	968	49	10.6	217	4	US-09-543-681A-8180	Sequence 8180, App
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901	49.5	10.7	349	4	US-09-489-847-242	Sequence 242, App	974	49	10.6	256	3	US-08-719-758-2	Sequence 2, Appli
902	49.5	10.7	352	3	US-08-967-272-2	Sequence 2, Appli	975	49	10.6	256	3	US-09-119-827-2	Sequence 2, Appli
903	49.5	10.7	353	4	US-09-107-532A-5053	Sequence 5053, App	976	49	10.6	278	4	US-09-328-352-8219	Sequence 8219, App
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981	49	10.6	334	4	US-09-317-254-54	Sequence 54, Appl	1054	48.5	10.5	133	4	US-09-536-784-188	Sequence 188, App
982	49	10.6	341	4	US-09-800-170-4	Sequence 4, Appl	1055	48.5	10.5	134	4	US-09-328-352-4247	Sequence 4247, Ap
983	49	10.6	343	1	US-08-047-413-13	Sequence 13, Appl	1056	48.5	10.5	138	4	US-09-248-796A-27800	Sequence 27800, A
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990	49	10.6	354	2	US-08-407-804-21	Sequence 21, Appl	1063	48.5	10.5	184	4	US-08-956-171B-5201	Sequence 5201, Ap
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993	49	10.6	369	4	US-09-248-796A-23009	Sequence 23009, A	1066	48.5	10.5	191	3	US-08-468-576B-13	Sequence 13, Appl
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997	49	10.6	423	4	US-09-370-767-42072	Sequence 42072, A	1070	48.5	10.5	206	4	US-09-248-796A-21349	Sequence 21349, A
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1004	49	10.6	445	4	US-09-634-238-273	Sequence 273, App	1077	48.5	10.5	231	2	US-09-058-483-2	Sequence 2, Appli
1005	49	10.6	446	2	US-08-833-610-2	Sequence 2, Appli	1078	48.5	10.5	246	1	US-08-197-834-7	Sequence 7, Appli
1006	49	10.6	446	3	US-08-934-033A-5	Sequence 5, Appli	1079	48.5	10.5	246	4	US-09-248-796A-27053	Sequence 27053, A
1007	49	10.6	446	4	US-09-145-828A-23	Sequence 23, Appl	1080	48.5	10.5	246	4	US-09-933-999A-7	Sequence 7, Appli
1008	49	10.6	446	4	US-09-330-235-12	Sequence 12, Appl	1081	48.5	10.5	250	4	US-09-328-352-6520	Sequence 6520, Ap
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1010	49	10.6	446	4	US-09-903-456-30	Sequence 30, Appl	1083	48.5	10.5	258	1	US-07-990-301A-2	Sequence 2, Appli
1011	49	10.6	446	4	US-09-538-092-781	Sequence 781, App	1084	48.5	10.5	267	3	US-08-430-225A-20	Sequence 20, Appl
1012	49	10.6	447	4	US-09-439-261-46	Sequence 46, Appl	1085	48.5	10.5	267	4	US-09-795-380-20	Sequence 20, Appl
1013	49	10.6	447	4	US-09-227-613-10	Sequence 10, Appl	1086	48.5	10.5	271	4	US-09-540-236-3291	Sequence 3291, Ap
1014	49	10.6	453	4	US-09-543-681A-5871	Sequence 5871, Ap	1087	48.5	10.5	296	4	US-09-543-681A-6537	Sequence 6537, Ap
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556	63.5	13.7	832	14	US-10-280-340-660	Sequence 660, App
557	63.5	13.7	837	9	US-09-949-192-25	Sequence 25, Appl
558	63.5	13.7	853	11	US-09-964-956-30	Sequence 30, Appl
559	63.5	13.7	853	14	US-10-190-115-30	Sequence 30, Appl
560	63.5	13.7	853	15	US-10-369-072-30	Sequence 32, Appl
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562	63.5	13.7	876	14	US-10-190-115-6	Sequence 6, Appli
563	63.5	13.7	876	15	US-10-369-072-6	Sequence 6, Appli
564	63.5	13.7	1026	15	US-10-332-426-6	Sequence 218456, A
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567	63	13.6	592	14	US-10-104-047-3366	Sequence 9246, Ap
568	63	13.6	895	14	US-10-156-761-9246	Sequence 2168, Ap
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572	62.5	13.5	530	16	US-10-437-963-151634	Sequence 151634, A
573	62.5	13.5	746	16	US-10-437-963-151656	Sequence 1253, Ap
574	62	13.4	264	9	US-09-764-864-1253	Sequence 186251, A
575	62	13.4	420	16	US-10-437-963-186251	Sequence 12, Appl
576	62	13.4	1017	15	US-10-654-416-12	Sequence 14, Appl
577	62	13.4	1023	15	US-10-654-416-14	Sequence 8, Appli
578	62	13.4	1027	15	US-10-654-416-8	Sequence 23, Appl
579	62	13.4	1634	14	US-10-435-766-23	Sequence 242469, A
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587	61.5	13.3	789	9	US-09-850-351A-6	Sequence 90, Appl
588	61.5	13.3	789	14	US-10-099-285-90	Sequence 6, Appli
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593	61	13.2	237	13	US-10-025-380-1062	Sequence 1302, Ap
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597	61	13.2	241	14	US-10-106-698-5105	

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607	61	13.2	768	16	US-10-437-963-111810	Sequence 111810,	680	59	12.8	1742	16	US-10-689-082-4	Sequence 4, Appli
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647	59.5	12.9	275	14	US-10-323-069A-105	Sequence 105, App	720	58	12.6	774	9	US-09-833-435A-8	Sequence 8, Appli
648	59.5	12.9	280	17	US-10-425-115-255376	Sequence 255376,	721	58	12.6	774	14	US-10-375-720-8	Sequence 8, Appli
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653	59.5	12.9	916	15	US-10-282-122A-68769	Sequence 68769, A	726	58	12.6	1323	14	US-10-195-144-81	Sequence 81, Appl
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661	59	12.8	261	9	US-09-799-777-12	Sequence 12, Appl	734	57.5	12.4	344	14	US-10-104-047-3358	Sequence 3358, Ap
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746	57.5	12.4	789	14	US-10-099-285-92	Sequence 92, Appl	819	56.5	12.2	789	14	US-10-099-285-96	Sequence 96, Appl
747	57.5	12.4	789	14	US-10-099-285-98	Sequence 98, Appl	820	56.5	12.2	789	16	US-10-473-687-5	Sequence 5, Appl
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778	57	12.3	824	14	US-10-032-585-7131	Sequence 7131, Ap	852	56	12.1	287	14	US-10-290-631-6	Sequence 6, Appl
779	57	12.3	844	16	US-10-437-963-144289	Sequence 144289, A	853	56	12.1	287	14	US-10-290-631-8	Sequence 8, Appl
780	57	12.3	861	10	US-09-820-843A-109	Sequence 109, App	854	56	12.1	287	16	US-10-777-524-6	Sequence 6, Appl
781	57	12.3	886	13	US-10-002-309B-2	Sequence 2, Appl	855	56	12.1	287	16	US-10-777-524-8	Sequence 8, Appl
782	57	12.3	1070	15	US-10-282-122A-78305	Sequence 78305, A	856	56	12.1	322	9	US-09-925-302-791	Sequence 791, App
783	57	12.3	1088	14	US-10-032-585-7198	Sequence 7198, Ap	857	56	12.1	322	10	US-09-925-302-791	Sequence 791, App
784	57	12.3	1222	14	US-10-012-697-1568	Sequence 1568, Ap	858	56	12.1	322	15	US-10-264-049-2828	Sequence 2828, Ap
785	57	12.3	1578	16	US-10-437-963-172263	Sequence 172263, A	859	56	12.1	323	15	US-10-312-273-131	Sequence 131, App
786	57	12.3	1769	14	US-10-369-493-4234	Sequence 4234, Ap	860	56	12.1	323	17	US-10-784-880-30	Sequence 30, Appl
787	57	12.3	1969	17	US-10-425-115-344401	Sequence 344401, A	861	56	12.1	328	15	US-10-289-762-637	Sequence 637, App
788	57	12.3	2732	14	US-10-238-075-1119	Sequence 1119, Ap	862	56	12.1	355	15	US-10-424-599-145529	Sequence 145529, A
789	57	12.3	2802	9	US-09-808-602-81	Sequence 81, Appl	863	56	12.1	373	17	US-10-425-115-312524	Sequence 312524, A
790	57	12.3	2802	10	US-09-800-198-69	Sequence 69, Appl	864	56	12.1	393	16	US-10-437-963-141661	Sequence 141661, A
791	57	12.3	2802	15	US-10-072-012-489	Sequence 489, App	865	56	12.1	443	15	US-10-282-122A-70490	Sequence 70490, A
792	57	12.3	2834	14	US-10-085-959-252	Sequence 252, App	866	56	12.1	476	15	US-10-729-807-17	Sequence 17, Appl
793	56.5	12.2	53	10	US-09-764-891-3639	Sequence 3639, Ap	867	56	12.1	509	10	US-09-794-422-34	Sequence 34, Appl
794	56.5	12.2	105	16	US-10-437-963-102714	Sequence 102714, A	868	56	12.1	525	9	US-09-814-550-2	Sequence 2, Appl
795	56.5	12.2	128	15	US-10-424-599-258072	Sequence 258072, A	869	56	12.1	525	10	US-09-794-422-6	Sequence 6, Appl
796	56.5	12.2	145	15	US-10-424-599-239133	Sequence 239133, A	870	56	12.1	525	14	US-10-132-9208-27	Sequence 27, Appl
797	56.5	12.2	192	16	US-10-437-963-152724	Sequence 152724, A	871	56	12.1	525	14	US-10-311-840-1	Sequence 1, Appl
798	56.5	12.2	254	10	US-09-946-290-20	Sequence 20, Appl	872	56	12.1	525	15	US-10-438-181A-27	Sequence 27, Appl
799	56.5	12.2	310	15	US-10-424-599-281933	Sequence 281933, A	873	56	12.1	540	10	US-09-794-422-46	Sequence 46, Appl
800	56.5	12.2	333	14	US-10-285-403-42	Sequence 42, Appl	874	56	12.1	540	16	US-10-437-963-103746	Sequence 103746, A
801	56.5	12.2	334	15	US-10-389-566-2413	Sequence 2413, Ap	875	56	12.1	551	15	US-10-413-943-69	Sequence 69, Appl
802	56.5	12.2	334	15	US-10-412-699B-434	Sequence 434, App	876	56	12.1	556	10	US-09-794-422-8	Sequence 8, Appl
803	56.5	12.2	338	14	US-10-369-493-22732	Sequence 22732, A	877	56	12.1	574	15	US-10-282-122A-45685	Sequence 45685, A
804	56.5	12.2	349	16	US-10-437-963-160226	Sequence 160226, A	878	56	12.1	608	10	US-09-769-787-8	Sequence 8, Appl
805	56.5	12.2	444	9	US-09-815-242-5785	Sequence 5785, Ap	879	56	12.1	631	14	US-10-225-066A-974	Sequence 974, App
806	56.5	12.2	452	9	US-09-815-242-12781	Sequence 12781, A	880	56	12.1	631	15	US-10-374-780A-2472	Sequence 2472, Ap
807	56.5	12.2	493	15	US-10-282-122A-73217	Sequence 73217, A	881	56	12.1	640	15	US-10-425-114-56122	Sequence 56122, A
808	56.5	12.2	499	15	US-10-424-599-184420	Sequence 184420, A	882	56	12.1	695	14	US-10-104-047-2395	Sequence 2395, Ap
809	56.5	12.2	500	15	US-10-282-122A-75263	Sequence 75263, A	883	56	12.1	726	15	US-10-282-122A-68866	Sequence 68866, A
810	56.5	12.2	500	15	US-10-282-122A-76049	Sequence 76049, A	884	56	12.1	770	9	US-09-784-316-5	Sequence 5, Appl
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812	56.5	12.2	636	14	US-10-138-075-4	Sequence 4, Appl	886	56	12.1	770	16	US-10-778-301-5	Sequence 5, Appl
813	56.5	12.2	746	9	US-09-904-226-6	Sequence 6, Appl	887	56	12.1	835	15	US-10-259-194A-306	Sequence 306, App
814	56.5	12.2	789	9	US-09-904-226-2	Sequence 2, Appl	888	56	12.1	847	16	US-10-437-963-118741	Sequence 118741, A
815	56.5	12.2	789	9	US-09-904-226-4	Sequence 4, Appl	889	56	12.1	862	16	US-10-437-963-107344	Sequence 107344, A
816	56.5	12.2	789	14	US-10-099-285-78	Sequence 78, Appl	899	56	12.1	877	14	US-10-309-422-32	Sequence 32, Appl

890	56	12.1	923	14	US-10-369-493-1734	Sequence 1734, Ap	963	55.5	12.0	440	15	US-10-264-049-2376	Sequence 2376, Ap
891	56	12.1	926	14	US-10-309-422-36	Sequence 36, Appl	964	55.5	12.0	441	15	US-10-334-143-37	Sequence 37, Appl
892	56	12.1	960	15	US-10-389-566-2373	Sequence 2373, Ap	965	55.5	12.0	444	14	US-10-156-761-11870	Sequence 11870, A
893	56	12.1	961	14	US-10-309-422-40	Sequence 40, Appl	966	55.5	12.0	450	15	US-10-282-122A-56157	Sequence 56157, A
894	56	12.1	1042	14	US-10-309-422-8	Sequence 8, Appl	967	55.5	12.0	467	9	US-09-785-474-2	Sequence 2, Appl
895	56	12.1	1043	14	US-10-309-422-20	Sequence 20, Appl	968	55.5	12.0	467	9	US-09-785-474-4	Sequence 4, Appl
896	56	12.1	1091	14	US-10-309-422-12	Sequence 12, Appl	969	55.5	12.0	467	9	US-09-785-474-28	Sequence 28, Appl
897	56	12.1	1092	14	US-10-309-422-24	Sequence 24, Appl	970	55.5	12.0	467	9	US-09-785-474-30	Sequence 30, Appl
898	56	12.1	1093	14	US-10-309-422-24	Sequence 24, Appl	971	55.5	12.0	467	9	US-09-785-474-32	Sequence 32, Appl
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901	56	12.1	1126	14	US-10-309-422-16	Sequence 16, Appl	974	55.5	12.0	526	15	US-10-403-571-70	Sequence 70, Appl
902	56	12.1	1127	14	US-10-309-422-28	Sequence 28, Appl	975	55.5	12.0	616	14	US-10-372-686-7	Sequence 7, Appl
903	56	12.1	1363	14	US-10-032-585-7800	Sequence 7800, Ap	976	55.5	12.0	616	14	US-10-371-558-7	Sequence 7, Appl
904	56	12.1	1394	14	US-09-839-996-2	Sequence 2, Appl	977	55.5	12.0	616	14	US-10-300-453A-41	Sequence 41, Appl
905	56	12.1	1394	14	US-10-080-508-2	Sequence 2, Appl	978	55.5	12.0	616	14	US-10-375-553-7	Sequence 7, Appl
906	56	12.1	1394	15	US-10-645-655-2	Sequence 2, Appl	979	55.5	12.0	616	15	US-10-372-553-7	Sequence 7, Appl
907	56	12.1	1394	16	US-10-687-046-2	Sequence 2, Appl	980	55.5	12.0	621	15	US-10-424-599-217291	Sequence 217291, A
908	56	12.1	1468	15	US-10-282-122A-65027	Sequence 65027, A	981	55.5	12.0	728	15	US-10-282-122A-70944	Sequence 70944, A
909	56	12.1	1829	14	US-10-435-765-13	Sequence 13, Appl	982	55.5	12.0	814	16	US-10-437-963-139533	Sequence 139533, A
910	56	12.1	2633	14	US-10-144-194A-82	Sequence 82, Appl	983	55.5	12.0	1192	14	US-10-369-493-3502	Sequence 3502, Ap
911	56	12.1	2724	9	US-09-808-602-13	Sequence 13, Appl	984	55.5	12.0	1560	17	US-10-783-528-89	Sequence 89, Appl
912	56	12.1	2724	10	US-09-800-198-13	Sequence 13, Appl	985	55.5	12.0	1593	10	US-09-981-151A-30	Sequence 30, Appl
913	56	12.1	2733	9	US-09-808-602-8	Sequence 8, Appl	986	55.5	12.0	1593	14	US-10-295-027-1317	Sequence 1317, Ap
914	56	12.1	2733	10	US-09-800-198-8	Sequence 8, Appl	987	55.5	12.0	2076	16	US-10-437-963-137291	Sequence 1, Appl
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916	56	12.1	2764	10	US-09-800-198-68	Sequence 68, Appl	989	55.5	12.0	3241	15	US-10-647-057-1	Sequence 1, Appl
917	56	12.1	2765	9	US-10-072-012-487	Sequence 487, Appl	990	55.5	12.0	4660	15	US-10-464-368-74	Sequence 74, Appl
918	56	12.1	2765	10	US-09-808-602-84	Sequence 84, Appl	991	55.5	12.0	4660	15	US-10-437-963-130045	Sequence 130045, A
919	56	12.1	2765	10	US-09-800-198-72	Sequence 72, Appl	992	55.5	11.9	77	16	US-10-425-114-54224	Sequence 54224, A
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922	55.5	12.0	122	9	US-09-071-035-170	Sequence 170, Appl	995	55.5	11.9	94	15	US-10-424-599-149019	Sequence 247469, A
923	55.5	12.0	122	14	US-10-206-576-170	Sequence 170, Appl	996	55.5	11.9	105	17	US-10-425-115-247469	Sequence 264297, A
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925	55.5	12.0	130	16	US-10-767-701-42300	Sequence 42300, A	998	55.5	11.9	119	15	US-10-424-599-163523	Sequence 269019, A
926	55.5	12.0	138	15	US-10-424-599-172305	Sequence 172305, A	999	55.5	11.9	121	17	US-10-425-115-289019	Sequence 78, Appl
927	55.5	12.0	141	15	US-10-424-599-172305	Sequence 172305, A	1000	55.5	11.9	126	9	US-09-867-550-78	Sequence 212675, A
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929	55.5	12.0	131	15	US-10-424-599-172303	Sequence 172303, A	1002	55.5	11.9	182	16	US-10-437-963-201465	Sequence 231493, A
930	55.5	12.0	216	16	US-10-408-765A-1144	Sequence 1144, Ap	1003	55.5	11.9	183	15	US-10-424-599-231493	Sequence 224180, A
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932	55.5	12.0	217	16	US-10-408-765A-2763	Sequence 2763, Ap	1005	55.5	11.9	197	15	US-10-424-599-211817	Sequence 41574, A
933	55.5	12.0	223	16	US-10-767-701-51927	Sequence 51927, A	1006	55.5	11.9	201	16	US-10-767-701-415174	Sequence 286059, A
934	55.5	12.0	270	17	US-10-425-115-308893	Sequence 308893, A	1007	55.5	11.9	205	17	US-10-425-115-286059	Sequence 179626, A
935	55.5	12.0	321	9	US-09-920-068A-2	Sequence 2, Appl	1008	55.5	11.9	206	16	US-10-437-963-179626	Sequence 5479, Ap
936	55.5	12.0	321	11	US-09-801-944B-268	Sequence 268, Appl	1009	55.5	11.9	222	9	US-09-738-626-5479	Sequence 188389, A
937	55.5	12.0	321	14	US-10-188-405-2	Sequence 2, Appl	1010	55.5	11.9	252	16	US-10-437-963-188389	Sequence 320478, A
938	55.5	12.0	321	14	US-10-183-116-35	Sequence 35, Appl	1011	55.5	11.9	255	17	US-10-425-115-320478	Sequence 10568, A
939	55.5	12.0	321	14	US-10-079-384-8	Sequence 8, Appl	1012	55.5	11.9	263	14	US-10-369-493-10568	Sequence 33669, A
940	55.5	12.0	321	14	US-10-017-161-1050	Sequence 1050, Ap	1013	55.5	11.9	299	16	US-10-767-701-33669	Sequence 63113, A
941	55.5	12.0	321	14	US-10-258-768-1	Sequence 1, Appl	1014	55.5	11.9	300	16	US-10-695-499-182	Sequence 182, App
942	55.5	12.0	321	14	US-10-239-421-2	Sequence 2, Appl	1015	55.5	11.9	359	15	US-10-282-122A-63113	Sequence 63113, A
943	55.5	12.0	321	14	US-10-305-553-4	Sequence 4, Appl	1016	55.5	11.9	364	14	US-10-369-493-23502	Sequence 23502, A
944	55.5	12.0	321	14	US-10-088-726-19	Sequence 19, Appl	1017	55.5	11.9	369	14	US-10-319-130-19	Sequence 19, Appl
945	55.5	12.0	321	14	US-10-321-807-10	Sequence 10, Appl	1018	55.5	11.9	409	16	US-10-437-963-140981	Sequence 140981, A
946	55.5	12.0	321	14	US-10-237-467-8	Sequence 8, Appl	1019	55.5	11.9	420	15	US-10-225-067-4	Sequence 109143, A
947	55.5	12.0	321	14	US-10-182-822A-18	Sequence 18, Appl	1020	55.5	11.9	475	15	US-10-437-963-203850	Sequence 203850, A
948	55.5	12.0	321	15	US-10-343-650A-42	Sequence 42, Appl	1021	55.5	11.9	470	15	US-10-055-569A-41	Sequence 41, Appl
949	55.5	12.0	321	16	US-10-321-807-10	Sequence 10, Appl	1022	55.5	11.9	470	17	US-10-739-930-6014	Sequence 202009, A
950	55.5	12.0	321	16	US-10-314-048A-10	Sequence 10, Appl	1023	55.5	11.9	475	14	US-10-238-075-817	Sequence 817, App
951	55.5	12.0	337	17	US-10-425-115-194274	Sequence 194274, A	1024	55.5	11.9	531	15	US-10-425-114-46811	Sequence 46811, A
952	55.5	12.0	347	14	US-10-292-798-892	Sequence 892, App	1025	55.5	11.9	540	17	US-10-425-115-353220	Sequence 353220, A
953	55.5	12.0	356	17	US-10-425-115-359329	Sequence 359329, A	1026	55.5	11.9	551	15	US-10-413-943-66	Sequence 66, Appl
954	55.5	12.0	359	15	US-10-282-122A-53431	Sequence 53431, A	1027	55.5	11.9	551	16	US-10-437-963-203850	Sequence 203850, A
955	55.5	12.0	369	9	US-09-841-786-2	Sequence 2, Appl	1028	55.5	11.9	575	15	US-10-055-569A-41	Sequence 41, Appl
956	55.5	12.0	369	15	US-10-647-057-2	Sequence 2, Appl	1029	55.5	11.9	612	15	US-10-424-599-202009	Sequence 202009, A
957	55.5	12.0	388	9	US-09-734-300-8	Sequence 8, Appl	1030	55.5	11.9	622	16	US-10-695-499-185	Sequence 185, App
958	55.5	12.0	400	14	US-10-243-552-372	Sequence 372, App	1031	55.5	11.9	657	14	US-10-104-047-2529	Sequence 110515, A
959	55.5	12.0	400	14	US-10-243-552-853	Sequence 853, App	1032	55.5	11.9	659	16	US-10-437-963-110515	Sequence 51723, A
960	55.5	12.0	422	15	US-10-425-114-53904	Sequence 53904, A	1033	55.5	11.9	665	15	US-10-282-122A-51723	Sequence 24, Appl
961	55.5	12.0	436	15	US-10-282-122A-67746	Sequence 67746, A	1034	55.5	11.9	704	10	US-10-362-327-24	Sequence 11, Appl
962	55.5	12.0	437	14	US-10-369-493-6271	Sequence 6271, Ap	1035	55.5	11.9				

1036	55	11.9	704	14	US-10-238-977A-11	Sequence 11, Appl	1109	54.5	11.8	819	15	US-10-412-862-10	Sequence 10, Appl
1037	55	11.9	706	15	US-10-413-943-61	Sequence 61, Appl	1110	54.5	11.8	826	10	US-09-769-787-194	Sequence 194, App
1038	55	11.9	759	14	US-10-032-585-7880	Sequence 7880, App	1111	54.5	11.8	838	10	US-09-884-465A-8	Sequence 8, Appl
1039	55	11.9	824	16	US-10-467-595-4	Sequence 4, Appl	1112	54.5	11.8	838	14	US-10-324-143-9	Sequence 9, Appl
1040	55	11.9	863	15	US-10-282-122A-76063	Sequence 76063, A	1113	54.5	11.8	838	15	US-10-412-850-4	Sequence 4, Appl
1041	55	11.9	883	15	US-10-282-122A-42626	Sequence 42626, A	1114	54.5	11.8	838	15	US-10-387-783-4	Sequence 4, Appl
1042	55	11.9	1045	16	US-10-437-963-113258	Sequence 113258, A	1115	54.5	11.8	838	15	US-10-412-862-4	Sequence 4, Appl
1043	55	11.9	1250	15	US-10-112-944-249	Sequence 249, App	1116	54.5	11.8	1046	14	US-10-369-493-1547	Sequence 1547, App
1044	55	11.9	1953	15	US-10-282-122A-43730	Sequence 43730, A	1117	54.5	11.8	1069	15	US-10-424-599-259331	Sequence 259331, App
1045	55	11.9	2273	15	US-10-282-122A-66115	Sequence 66115, A	1118	54.5	11.8	1069	15	US-10-424-599-259331	Sequence 259331, App
1046	54.5	11.8	75	16	US-10-437-963-110009	Sequence 110009, A	1119	54.5	11.8	1373	14	US-10-032-585-7129	Sequence 7129, App
1047	54.5	11.8	87	15	US-10-276-774-1709	Sequence 1709, App	1119	54.5	11.8	1373	14	US-10-087-464-10	Sequence 10, Appl
1048	54.5	11.8	90	17	US-10-425-115-367248	Sequence 367248, A	1120	54.5	11.8	2108	14	US-10-369-493-1537	Sequence 1537, App
1049	54.5	11.8	94	16	US-10-437-963-134784	Sequence 134784, A	1121	54.5	11.8	2344	9	US-09-815-242-12713	Sequence 12713, A
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1053	54.5	11.8	188	15	US-10-424-599-160446	Sequence 160446, A	1125	54	11.7	74	16	US-09-864-408A-6436	Sequence 6436, A
1054	54.5	11.8	213	15	US-10-424-599-265300	Sequence 265300, A	1126	54	11.7	74	16	US-10-767-701-55034	Sequence 55034, A
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1328	53.5	11.6	761	9	US-09-147-947-4	Sequence 4, Appli	1401	53	11.5	425	15	US-10-112-944-441	Sequence 441, App
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1331	53.5	11.6	808	16	US-10-437-963-127142	Sequence 127142, A	1404	53	11.5	441	15	US-10-425-114-62170	Sequence 62170, A
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1334	53.5	11.6	1023	14	US-09-884-696-5	Sequence 5, Appli	1407	53	11.5	446	9	US-09-815-242-5418	Sequence 5418, Ap
1335	53.5	11.6	1036	14	US-10-193-764-69	Sequence 69, Appl	1408	53	11.5	453	9	US-09-815-242-12562	Sequence 12562, A
1336	53.5	11.6	1113	17	US-10-739-930-5799	Sequence 5799, Ap	1409	53	11.5	459	14	US-10-369-493-20977	Sequence 20977, A
1337	53.5	11.6	1477	13	US-10-092-880-4	Sequence 4, Appli	1410	53	11.5	462	14	US-10-369-493-568	Sequence 568, App
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1361	53	11.5	123	14	US-10-104-473A-24	Sequence 24, Appl							
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1366	53	11.5	148	15	US-10-424-599-156680	Sequence 156680, A							
1367	53	11.5	157	17	US-10-425-115-237454	Sequence 237454, A							
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1369	53	11.5	160	15	US-10-424-599-194908	Sequence 194908, A							
1370	53	11.5	162	17	US-10-425-115-187794	Sequence 187794, A							
1371	53	11.5	163	16	US-10-767-701-60211	Sequence 60211, A							
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1373	53	11.5	184	17	US-10-739-930-7377	Sequence 7377, Ap							
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1376	53	11.5	200	15	US-10-425-114-595861	Sequence 59586, A							
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1383	53	11.5	270	13	US-10-029-180-20	Sequence 20, Appl							
1384	53	11.5	273	15	US-10-425-114-69295	Sequence 69295, A							
1385	53	11.5	290	14	US-10-106-698-5388	Sequence 5388, Ap							
1386	53	11.5	303	17	US-10-425-115-355932	Sequence 355932, A							
1387	53	11.5	327	15	US-10-282-122A-55729	Sequence 55729, A							
1388	53	11.5	328	14	US-10-171-404A-32	Sequence 32, Appl							
1389	53	11.5	328	14	US-10-225-066A-542	Sequence 542, App							
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1392	53	11.5	331	14	US-10-102-806-606	Sequence 606, App							
1393	53	11.5	333	15	US-10-282-122A-50441	Sequence 50441, A							
1394	53	11.5	342	17	US-10-425-115-223912	Sequence 223912, A							
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1397	53	11.5	393	15	US-10-425-114-68386	Sequence 68386, A							
1398	53	11.5	401	15	US-10-425-114-43248	Sequence 43248, A							
1399	53	11.5	403	16	US-10-767-701-44078	Sequence 44078, A							
1400	53	11.5	425	14	US-10-168-066-2	Sequence 2, Appli							

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Job time : 104 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
OM protein - protein search, using sw model
Run on: December 3, 2004, 05:08:11 ; Search time 68 Seconds
      (without alignments)
      474.789 Million cell updates/sec

Title: US-09-997-653-377
Perfect score: 462
Sequence: 1 MTFPLSLLLLVCEAIRSN.....DSRGLILGAEWGRGVKKNT 90
Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5
Searched: 2002273 seqs, 358729299 residues
Total number of hits satisfying chosen parameters: 2002273
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 1500 summaries
Database : 1: geneseqp1980s.*
           2: geneseqp1990s.*
           3: geneseqp2000s.*
           4: geneseqp2001s.*
           5: geneseqp2002s.*
           6: geneseqp2003as.*
           7: geneseqp2003bs.*
           8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
SUMMARIES

No. Score Match Length DB ID Description
RESULT 1
ID AAY66748 standard; protein; 90 AA.
DE Membrane-bound protein PRO1159.
PN W09963088-A2.
PD 09-DEC-1999.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 462; DB 3; Length 90;
  Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 2
ID AAB33469 standard; protein; 90 AA.
DE Human PRO1159 protein UNQ589 SEQ ID NO:273.
PN W0200053758-A2.
PD 14-SEP-2000.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 462; DB 3; Length 90;
  Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 3
ID AAU12408 standard; protein; 90 AA.
DE Human PRO1159 polypeptide sequence.
PN W0200140466-A2.
PD 07-JUN-2001.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 462; DB 4; Length 90;
  Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 4
ID AAB50922 standard; protein; 90 AA.
DE Human PRO1159 protein.
PN W0200073452-A2.
PD 07-DEC-2000.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 462; DB 4; Length 90;
  Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 5
ID AAB65271 standard; protein; 90 AA.
DE Human PRO1159 (UNQ589) protein sequence SEQ ID NO:377.
PN W0200073454-A1.
PD 07-DEC-2000.
PA (GETH ) GENENTECH INC.
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  Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 6
ID AAB66806 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 462; DB 6; Length 90;
  Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 7
ID ABU59164 standard; protein; 90 AA.
DE Novel human secreted or transmembrane protein PRO1159.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 462; DB 6; Length 90;
  Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 8
ID ABU82676 standard; protein; 90 AA.
DE Human secreted/transmembrane protein PRO1159.
PN US2003032023-A1.
PD 13-FEB-2003.
  Query Match 100.0%; Score 462; DB 6; Length 90;
  Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 9
ID ABO17852 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 462; DB 6; Length 90;
  Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 10
ID ABU60595 standard; protein; 90 AA.
DE Human secreted/transmembrane protein, #154.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 462; DB 6; Length 90;
  Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 11
ID ABU13977 standard; protein; 90 AA.
DE Human PRO1159 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH ) GENENTECH LTD.
  Query Match 100.0%; Score 462; DB 6; Length 90;
  Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 12
ID ABU81106 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 462; DB 6; Length 90;
  Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 13
ID ABU72562 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 462; DB 6; Length 90;
  Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 14
ID ABU66806 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 462; DB 6; Length 90;
  Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 15
ID ABU59887 standard; protein; 90 AA.
DE Novel secreted and transmembrane protein PRO1159.
PN US2003017563-A1.
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PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 6; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 16
ID ABUS9311 standard; protein; 90 AA.
DE Human secreted/transmembrane protein, #154.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 462; DB 6; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 17
ID ABO26008 standard; protein; 90 AA.
DE Human PRO1159 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 6; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 18
ID ABO25077 standard; protein; 90 AA.
DE Human secreted/transmembrane protein (PRO) #237.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 6; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 19
ID ABUS9017 standard; protein; 90 AA.
DE Human secreted/transmembrane protein, #154.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 6; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 20
ID ABUS92395 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 462; DB 6; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 21
ID ABUS9460 standard; protein; 90 AA.
DE Novel human secreted or transmembrane protein PRO1124.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 462; DB 6; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 22
ID ABU67082 standard; protein; 90 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 474.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 6; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 23
ID ABUS2226 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 462; DB 6; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 24
ID ABU10932 standard; protein; 90 AA.
DE Human PRO polypeptide #118.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 6; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 25

ID ABU81684 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 6; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 26
ID ABUS8623 standard; protein; 90 AA.
DE Human secreted and transmembrane polypeptide PRO1159.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 6; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 27
ID ABO34137 standard; protein; 90 AA.
DE Human PRO1159 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 462; DB 6; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 28
ID ADA45993 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 6; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 29
ID ADA76424 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 6; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 30
ID ADA19074 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 6; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 31
ID ADA61697 standard; protein; 90 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 6; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 32
ID ADB19482 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003058796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 6; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 33
ID ADB28023 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 6; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 34
ID ADA86502 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.

[illegible][illegible]

[illegible]

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PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 72
DE Human PRO polypeptide #237.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 73
ID ADA61134 standard; protein; 90 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 74
ID ADB24281 standard; protein; 90 AA.
DE Human PRO polypeptide SEQ ID NO 474.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 462; DB 6; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 75
ID ADA96610 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 462; DB 6; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 76
ID ADA81182 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 77
ID ADA96058 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
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RESULT 78
ID ADB26367 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 462; DB 6; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 79
ID ADB21852 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 80
ID ADA77631 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 81
ID ADB18371 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 82
ID ADA87054 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 83
ID ADA88157 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 84
ID ADA46545 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 85
ID ADB28575 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 86
ID ADB29127 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 87
ID ABO53223 standard; protein; 90 AA.
DE Human secreted/transmembrane protein PRO1159.
PN US2003044806-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 88
ID ADA77079 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 89
ID ADA22500 standard; protein; 90 AA.
DE Human secreted/transmembrane polypeptide PRO1159.
PN US2003040473-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 90
ID ADA88709 standard; protein; 90 AA.
```

DE Novel human secreted and transmembrane protein PROI159.
PN US2003073213-A1.
PD 17-APR-2003.

PA (GETH) GENENTECH INC.
Query Match Similarity 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;

RESULT 91

ID ADA97714 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003082686-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match Similarity 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;

RESULT 92

ID ADB27471 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003022239-A1.
PD 30-JAN-2003.

Query Match Similarity 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;

RESULT 93

ID ADB22404 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PROI159.
PN US2003087344-A1.
PD 08-MAY-2003.

Query Match Similarity 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;

RESULT 94

ID ABO22593 standard; protein; 90 AA.
DE Human secreted/transmembrane protein PROI159.
PN US2003017982-A1.
PD 23-JAN-2003.

Query Match Similarity 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;

RESULT 95

ID ADA06666 standard; protein; 90 AA.
DE Human secreted/transmembrane PRO polypeptide #118.
PN US2003049638-A1.
PD 13-MAR-2003.

Query Match Similarity 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;

RESULT 96

ID ADA39359 standard; protein; 90 AA.
DE Human secreted/transmembrane protein PROI159.
PN US2003059782-A1.
PD 27-MAR-2003.

Query Match Similarity 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;

RESULT 97

ID ADA67095 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003068793-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match Similarity 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;

RESULT 98

ID ADB22956 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003077711-A1.
PD 24-APR-2003.

PA (GETH) GENENTECH INC.
Query Match Similarity 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;

RESULT 99

ID ADB23729 standard; protein; 90 AA.
DE Human PRO polypeptide SEQ ID NO 474.
PN US2003077712-A1.
PD 24-APR-2003.

PA (GETH) GENENTECH INC.
Query Match Similarity 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;

RESULT 99

ID ADB23729 standard; protein; 90 AA.
DE Human PRO polypeptide SEQ ID NO 474.
PN US2003077712-A1.
PD 24-APR-2003.

PA (GETH) GENENTECH INC.
Query Match Similarity 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;

RESULT 100
ID ADA92451 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PROI159.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 101
ID ADB15514 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 102
ID ADB38766 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PROI159.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 103
ID ADB96385 standard; protein; 90 AA.
DE Human PRO polypeptide #118.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 104
ID ADB38214 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PROI159.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 105
ID ADB66686 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PROI159.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 106
ID ADB89766 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 107
ID ADB90498 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 108
ID ADB39599 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PROI159.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 109
ID ADB47222 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PROI159.

DE Novel human secreted and transmembrane protein PRO1159.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 110
ID ADB86829 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 111
ID ADB77434 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 112
ID ADB34591 standard; protein; 90 AA.
DE Human PRO polypeptide SEQ ID NO 474.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 113
ID ADB35695 standard; protein; 90 AA.
DE Human PRO polypeptide SEQ ID NO 474.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 114
ID ADB34039 standard; protein; 90 AA.
DE Human PRO polypeptide SEQ ID NO 474.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 115
ID ADB35143 standard; protein; 90 AA.
DE Human PRO polypeptide SEQ ID NO 474.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 116
ID ADB36247 standard; protein; 90 AA.
DE Human PRO polypeptide SEQ ID NO 474.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 117
ID ADB46642 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 118
ID ADC57857 standard; protein; 90 AA.
DE Human PRO polypeptide #118.

PN US2003027754-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 119
ID ADC55221 standard; protein; 90 AA.
DE Human PRO polypeptide #118.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 120
ID ADC12088 standard; protein; 90 AA.
DE Human secreted/transmembrane protein PRO1159.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 121
ID ADC56510 standard; protein; 90 AA.
DE Human PRO polypeptide #118.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 122
ID ADC07565 standard; protein; 90 AA.
DE Human secreted/transmembrane protein PRO1159.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 123
ID ADC11555 standard; protein; 90 AA.
DE Human secreted/transmembrane protein PRO1159.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 124
ID ADC50515 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 125
ID ADC72062 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 126
ID ADC60041 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 127
ID ADC53048 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein Seg ID474.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 128
ID ADC57402 standard; protein; 90 AA.

DE Novel human secreted and transmembrane protein Seq ID474.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 462; DB 7; Length 90;
Pred. No. 1.3e-48;
RESULT 129
ID ADC60593 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 462; DB 7; Length 90;
Pred. No. 1.3e-48;
RESULT 130
ID ADC51068 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 462; DB 7; Length 90;
Pred. No. 1.3e-48;
RESULT 131
ID ADC65595 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 462; DB 7; Length 90;
Pred. No. 1.3e-48;
RESULT 132
ID ADC54693 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein Seq ID474.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 462; DB 7; Length 90;
Pred. No. 1.3e-48;
RESULT 133
ID ADC53654 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein Seq ID474.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 462; DB 7; Length 90;
Pred. No. 1.3e-48;
RESULT 134
ID ADC59177 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein Seq ID474.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 462; DB 7; Length 90;
Pred. No. 1.3e-48;
RESULT 135
ID ADC56055 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein Seq ID474.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 462; DB 7; Length 90;
Pred. No. 1.3e-48;
RESULT 136
ID ADC58625 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein Seq ID474.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 462; DB 7; Length 90;
Pred. No. 1.3e-48;
RESULT 137
ID ADC14677 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.

PN US2003082546-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 462; DB 7; Length 90;
Pred. No. 1.3e-48;
RESULT 138
ID ADD08209 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 462; DB 7; Length 90;
Pred. No. 1.3e-48;
RESULT 139
ID ADD03299 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 462; DB 7; Length 90;
Pred. No. 1.3e-48;
RESULT 140
ID ADC90291 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 462; DB 7; Length 90;
Pred. No. 1.3e-48;
RESULT 141
ID ADC82034 standard; protein; 90 AA.
DE Human PRO polypeptide #118.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 462; DB 7; Length 90;
Pred. No. 1.3e-48;
RESULT 142
ID ADC69710 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 462; DB 7; Length 90;
Pred. No. 1.3e-48;
RESULT 143
ID ADC48599 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 462; DB 7; Length 90;
Pred. No. 1.3e-48;
RESULT 144
ID ADD10128 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 462; DB 7; Length 90;
Pred. No. 1.3e-48;
RESULT 145
ID ADD07676 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 462; DB 7; Length 90;
Pred. No. 1.3e-48;
RESULT 146
ID ADD04703 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 462; DB 7; Length 90;
Pred. No. 1.3e-48;

Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 147
ID ADC82567 standard; protein; 90 AA.
DE Human PRO polypeptide #118.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 148
ID ADC80659 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 149
ID ADD11166 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 150
ID ADC48047 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 151
ID ADD08747 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 152
ID ADC80107 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 153
ID ADD06996 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 154
ID ADD09576 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 155
ID ADC83243 standard; protein; 90 AA.
DE Human PRO polypeptide #118.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 156
ID ADD41289 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.

PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 157
ID ADD52428 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 158
ID ADD53168 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 159
ID ADD53720 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 160
ID ADD55350 standard; protein; 90 AA.
DE Human PRO polypeptide #118.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 161
ID ADD56308 standard; protein; 90 AA.
DE Human PRO polypeptide #118.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 162
ID ADD51876 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 163
ID ADD02675 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 164
ID ADD02109 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 165
ID ADD54291 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 166
ID ADD54746 standard; protein; 90 AA.
DE Human PRO polypeptide #118.
PN US2002132253-Al.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 167
ID ADD92608 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003199030-Al.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 168
ID ADD91504 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003199055-Al.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 169
ID ADE04118 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003199057-Al.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 170
ID ADE26900 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003087304-Al.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 171
ID ADE32415 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003194765-Al.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 172
ID ADE22347 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003199056-Al.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 173
ID ADD79571 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003203428-Al.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 174
ID ADE42107 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003194772-Al.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;

RESULT 175
ID ADE17924 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003199023-Al.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 176
ID ADD92056 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003199053-Al.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 177
ID ADE33519 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003194767-Al.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 178
ID ADE34071 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003194791-Al.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 179
ID ADD80123 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003207417-Al.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 180
ID ADD93160 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003194768-Al.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 181
ID ADE19580 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003199025-Al.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 182
ID ADE19028 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003199026-Al.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 183
ID ADE43224 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003199033-Al.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 184

ADP96013 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PD US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 185
ID ADE22899 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PD US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 186
ID ADD79017 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PD US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 187
ID ADE26367 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PD US2003087305-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 188
ID ADE32967 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PD US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 189
ID ADE42659 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PD US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 190
ID ADD80675 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PD US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 191
ID ADD89703 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PD US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 192
ID ADE40987 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PD US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 193
ID ADE04786 standard; protein; 90 AA.
DE Human PRO polypeptide #237.

PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 194
ID ADE92915 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PD US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 195
ID ADE67304 standard; protein; 90 AA.
DE Human PRO1159 amino acid sequence SEQ ID NO:377.
PD US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 196
ID ADG21624 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PD US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 197
ID ADG23265 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PD US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 198
ID ADE97600 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PD US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 199
ID ADG80664 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PD US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 200
ID ADG80112 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PD US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 201
ID ADH5404 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PD US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 202
ID ADH5956 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PD US2003207379-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 203
ID ADI3558 standard; protein; 90 AA.
DE Human PRO polypeptide #118.
PD US2003050457-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 204
ID ADI64175 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PD US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 205
ID ADI65124 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PD US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 206
ID ADI63623 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PD US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 207
ID ADH82037 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PD US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 208
ID ADI00051 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PD US2003049682-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 209
ID ADH81485 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PD US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 210
ID ADM82654 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PD US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 211
ID ADN16053 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PD US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 212
ID ADN16682 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PD US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 213
ID ADN15501 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PD US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 214
ID ADN14949 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PD US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 215
ID ADC81211 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PD US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 216
ID ADD76659 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PD US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 217
ID ADD88023 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PD US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 218
ID ADD86427 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PD US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 219
ID ADE75875 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PD US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 220
ID ADE23451 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PD US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;

PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 240
ID ADF98152 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 241
ID ADG24369 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 242
ID ADF98723 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 243
ID ADG03554 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 244
ID ADF99275 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 245
ID ADG16860 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 246
ID ADG05319 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 247
ID ADG19586 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 248
ID ADG13423 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003207357-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 249
ID ADG08480 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 250
ID ADG15650 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 251
ID ADF97048 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 252
ID ADG06233 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 253
ID ADG23817 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 254
ID ADG04106 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 255
ID ADG25007 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 256
ID ADG07304 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 257
ID ADG07856 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003207356-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 258
ID ADG55351 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003194778-A1.
PD 16-OCT-2003
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 259
ID ADG61015 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003207390-A1.
PD 06-NOV-2003
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 260
ID ADG62119 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003207428-A1.
PD 06-NOV-2003
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 261
ID ADG82320 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003207358-A1.
PD 06-NOV-2003
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 262
ID ADG57559 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003207362-A1.
PD 06-NOV-2003
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 263
ID ADG57007 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003207364-A1.
PD 06-NOV-2003
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 264
ID ADG55903 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003207365-A1.
PD 06-NOV-2003
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 265
ID ADG58663 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003207368-A1.
PD 06-NOV-2003
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 266
ID ADG71029 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003207420-A1.
PD 06-NOV-2003
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 267
ID ADG58111 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003207363-A1.
PD 06-NOV-2003
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 268
ID ADG53695 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003207415-A1.
PD 06-NOV-2003
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 269
ID ADG71581 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003207421-A1.
PD 06-NOV-2003
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 270
ID ADG81768 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003207805-A1.
PD 06-NOV-2003
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 271
ID ADH19623 standard; protein; 90 AA.
DE Human secreted/transmembrane protein PRO1159.
PN US2003228656-A1.
PD 11-DEC-2003
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 272
ID ADH30730 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003077723-A1.
PD 24-APR-2003
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 273
ID ADH12097 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003207419-A1.
PD 06-NOV-2003
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 274
ID ADG52519 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003207414-A1.
PD 06-NOV-2003
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 275
ID ADG54247 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003207416-A1.
PD 06-NOV-2003
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;

RESULT 276
ID ADG81216 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 277
ID ADG56455 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 278
ID ADH12721 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 279
ID ADH21116 standard; protein; 90 AA.
DE Human secreted/transmembrane protein PRO1159.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 280
ID ADG61567 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 281
ID ADH20156 standard; protein; 90 AA.
DE Human secreted/transmembrane protein PRO1159.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 282
ID ADH28654 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 283
ID ADG54799 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 284
ID ADG59839 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 285
ID ADI61263 standard; protein; 90 AA.

DE Human PRO polypeptide #237.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 286
ID ADG10006 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 287
ID ADI15477 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 288
ID ADG09354 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 289
ID ADI14809 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 290
ID ADI18404 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 291
ID ADJ63685 standard; protein; 90 AA.
DE Novel human secreted and transmembrane protein PRO1159.
PN US20040319164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 292
ID ADJ77580 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 293
ID ADJ65702 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 462; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
RESULT 294
ID ADM27838 standard; protein; 90 AA.
DE Human PRO polypeptide #237.

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PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 462; DB 8; Length 90;
RESULT 295
ID ADM42562 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 462; DB 8; Length 90;
RESULT 296
ID ADM28424 standard; protein; 90 AA.
DE Human PRO polypeptide #237.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 462; DB 8; Length 90;
RESULT 297
ID AAU19838 standard; protein; 222 AA.
DE Human novel extracellular matrix protein, Seq ID No 488.
PN WO200155368-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 80.6%; Score 247.5; DB 4; Length 222;
RESULT 298
ID ABP48058 standard; protein; 222 AA.
DE Human polypeptide SEQ ID NO 488.
PN US2002042386-A1.
PD 11-APR-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match
Best Local Similarity 80.6%; Score 247.5; DB 5; Length 222;
RESULT 299
ID ADC11020 standard; protein; 222 AA.
DE Human protein from extracellular matrix gene 66 #2.
PN US2003059875-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 80.6%; Score 247.5; DB 7; Length 222;
RESULT 300
ID AAY27448 standard; protein; 247 AA.
DE Human SDCMP4 polypeptide.
PN WO9947673-A2.
PD 23-SEP-1999.
PA (SCHE ) SCHERING CORP.
Query Match
Best Local Similarity 80.6%; Score 247.5; DB 2; Length 247;
RESULT 301
ID AAW73989 standard; protein; 247 AA.
DE Human DC3' protein sequence.
PN JP11001497-A.
PD 06-JAN-1999.
PA (TAKE ) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity 80.6%; Score 247.5; DB 2; Length 247;
RESULT 302
ID ABB82496 standard; protein; 247 AA.
DE LIR-J24-2 polypeptide.
PN WO20027216-A2.
PD 03-OCT-2002.
PA (NOVS ) NOVARTIS AG.
Query Match
Best Local Similarity 53.6%; Score 247.5; DB 6; Length 247;
RESULT 303
ID ABB2842 standard; protein; 247 AA.
DE Human Dectin-1 polypeptide.
PN WO200296945-A2.
PD 05-DEC-2002.
PA (TSIS-) ISIS INNOVATION LTD.
Query Match
Best Local Similarity 61.7%; Score 143.5; DB 6; Length 244;
RESULT 304
ID AAW63012 standard; protein; 176 AA.
DE Mouse dectin-1 extracellular domain.
PN WO9828332-A2.
PD 02-JUL-1998.
PA (TEXA ) UNIV TEXAS SYSTEM.
Query Match
Best Local Similarity 62.2%; Score 139.5; DB 2; Length 176;
RESULT 305
ID ABB82498 standard; protein; 46 AA.
DE LIR-J24-stalk peptide.
PN WO20027216-A2.
PD 03-OCT-2002.
PA (NOVS ) NOVARTIS AG.
Query Match
Best Local Similarity 100.0%; Score 238; DB 6; Length 46;
RESULT 306
ID AAW63009 standard; protein; 244 AA.
DE Mouse dectin-1.
PN WO9828332-A2.
PD 02-JUL-1998.
PA (TEXA ) UNIV TEXAS SYSTEM.
Query Match
Best Local Similarity 31.1%; Score 143.5; DB 2; Length 244;
RESULT 307
ID ABB82844 standard; protein; 244 AA.
DE Mouse Dectin-1 polypeptide.
PN WO200296945-A2.
PD 05-DEC-2002.
PA (TSIS-) ISIS INNOVATION LTD.
Query Match
Best Local Similarity 31.1%; Score 143.5; DB 6; Length 244;
RESULT 308
ID AAW63012 standard; protein; 176 AA.
DE Mouse dectin-1 extracellular domain.
PN WO9828332-A2.
PD 02-JUL-1998.
PA (TEXA ) UNIV TEXAS SYSTEM.
Query Match
Best Local Similarity 62.2%; Score 139.5; DB 2; Length 176;
RESULT 309
ID AAW62936 standard; protein; 180 AA.
DE Mouse dectin-1 His-tagged extracellular domain.
PN WO9828332-A2.
PD 02-JUL-1998.
PA (TEXA ) UNIV TEXAS SYSTEM.
Query Match
Best Local Similarity 27.8%; Score 128.5; DB 2; Length 180;
RESULT 310
ID ABG10369 standard; protein; 274 AA.
DE Novel human diagnostic protein #10360.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 29.6%; Score 74.5; DB 4; Length 274;
RESULT 311
ID ABG24071 standard; protein; 274 AA.
DE Novel human diagnostic protein #24062.
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PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 16.1%; Score 74.5; DB 4; Length 274;
Best Local Similarity 29.6%; Pred. No. 2.7;
RESULT 312
ID ABB66222 standard; protein; 734 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 25458.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 15.2%; Score 70; DB 4; Length 734;
Best Local Similarity 31.7%; Pred. No. 39;
RESULT 313
ID AAW88755 standard; protein; 171 AA.
DE Secreted protein encoded by gene 173 clone HE8MG65.
PN WO9854963-A2.
PD 10-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.0%; Score 69.5; DB 2; Length 171;
Best Local Similarity 31.8%; Pred. No. 5.8;
RESULT 314
ID ABB50533 standard; protein; 171 AA.
DE Human secreted protein encoded by gene 173 SEQ ID NO:481.
PN WO200162891-A2.
PD 30-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.0%; Score 69.5; DB 4; Length 171;
Best Local Similarity 31.8%; Pred. No. 5.8;
RESULT 315
ID ABO44790 standard; protein; 171 AA.
DE Novel human secreted protein #233.
PN US2003065160-A1.
PD 03-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.0%; Score 69.5; DB 6; Length 171;
Best Local Similarity 31.8%; Pred. No. 5.8;
RESULT 316
ID ABO26270 standard; protein; 171 AA.
DE Human protein from novel secreted protein gene 173 #2.
PN US6525174-B1.
PD 25-FEB-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.0%; Score 69.5; DB 7; Length 171;
Best Local Similarity 31.8%; Pred. No. 5.8;
RESULT 317
ID AAW88706 standard; protein; 257 AA.
DE Secreted protein encoded by gene 173 clone HE8MG65.
PN WO9854963-A2.
PD 10-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.0%; Score 69.5; DB 2; Length 257;
Best Local Similarity 31.8%; Pred. No. 10;
RESULT 318
ID ABB50473 standard; protein; 257 AA.
DE Human secreted protein encoded by gene 173 SEQ ID NO:421.
PN WO200162891-A2.
PD 30-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.0%; Score 69.5; DB 4; Length 257;
Best Local Similarity 31.8%; Pred. No. 10;
RESULT 319
ID ABO44730 standard; protein; 257 AA.
DE Novel human secreted protein #173.
PN US2003065160-A1.
PD 03-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.0%; Score 69.5; DB 6; Length 257;
Best Local Similarity 31.8%; Pred. No. 10;
RESULT 320
ID ABO26210 standard; protein; 257 AA.
DE Human protein from novel secreted protein gene 173.
PN US6525174-B1.

PD 25-FEB-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.0%; Score 69.5; DB 7; Length 257;
Best Local Similarity 31.8%; Pred. No. 10;
RESULT 321
ID AAM93436 standard; protein; 265 AA.
DE Human polypeptide, SEQ ID NO: 3072.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 15.0%; Score 69.5; DB 4; Length 265;
Best Local Similarity 31.8%; Pred. No. 11;
RESULT 322
ID AAB88592 standard; protein; 265 AA.
DE Human hydrophobic domain containing protein clone HP10715 #96.
PN WO200112660-A2.
PD 22-FEB-2001.
PA (SAGA) SAGAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
Query Match 15.0%; Score 69.5; DB 4; Length 265;
Best Local Similarity 31.8%; Pred. No. 11;
RESULT 323
ID AAB74606 standard; protein; 265 AA.
DE Human HTGM48-iso protein sequence SEQ ID NO:7.
PN CN1272541-A.
PD 08-NOV-2000.
PA (NANF-) NANFANG RES CENT STATE HUMAN GENE GROUP.
Query Match 15.0%; Score 69.5; DB 4; Length 265;
Best Local Similarity 31.8%; Pred. No. 11;
RESULT 324
ID ABP64739 standard; protein; 265 AA.
DE Human protein SEQ ID 399.
PN WO200259260-A2.
PD 01-AUG-2002.
PA (HYSE-) HYSEQ INC.
Query Match 15.0%; Score 69.5; DB 5; Length 265;
Best Local Similarity 31.8%; Pred. No. 11;
RESULT 325
ID ADL31039 standard; protein; 265 AA.
DE Human protein encoded by a full length cDNA clone SeqID 3072.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 15.0%; Score 69.5; DB 8; Length 265;
Best Local Similarity 31.8%; Pred. No. 11;
RESULT 326
ID AAW22212 standard; protein; 622 AA.
DE Rat transferrin receptor.
PN WO9715830-A1.
PD 01-MAY-1997.
PA (UUNY) UNIV NEW YORK STATE RES FOUND.
Query Match 14.8%; Score 68.5; DB 2; Length 622;
Best Local Similarity 27.6%; Pred. No. 47;
RESULT 327
ID ABP56713 standard; protein; 622 AA.
DE Rat CD71 protein SEQ ID NO:26.
PN WO2002100336-A2.
PD 19-DEC-2002.
PA (TARG-) TARGET PROTEIN TECHNOLOGIES INC.
Query Match 14.8%; Score 68.5; DB 6; Length 622;
Best Local Similarity 27.6%; Pred. No. 47;
RESULT 328
ID ABU49494 standard; protein; 280 AA.
DE Protein encoded by Prokaryotic essential gene #35021.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 14.7%; Score 68; DB 6; Length 280;
Best Local Similarity 25.3%; Pred. No. 18;
RESULT 329
ID AAG25778 standard; protein; 343 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 29980.
PN EP1033405-A2.

PD 06-SEP-2000.
Query Match 14.6%; Score 67.5; DB 3; Length 343;
Best Local Similarity 24.3%; Pred. No. 27;
RESULT 330
ID ABG14367 standard; protein; 441 AA.
DE Novel human diagnostic protein #14358.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 14.6%; Score 67.5; DB 4; Length 441;
Best Local Similarity 27.6%; Pred. No. 39;
RESULT 331
ID ABO84145 standard; protein; 354 AA.
DE Pseudomonas aeruginosa polypeptide #16320.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 14.4%; Score 66.5; DB 7; Length 354;
Best Local Similarity 25.7%; Pred. No. 38;
RESULT 332
ID ADB06106 standard; protein; 527 AA.
DE Alloiococcus ostitis antigenic protein SEQ ID NO:46.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Query Match 14.4%; Score 66.5; DB 6; Length 527;
Best Local Similarity 30.6%; Pred. No. 66;
RESULT 333
ID ADB06108 standard; protein; 528 AA.
DE Alloiococcus ostitis antigenic protein SEQ ID NO:48.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Query Match 14.3%; Score 66; DB 4; Length 417;
Best Local Similarity 23.8%; Pred. No. 55;
RESULT 334
ID AAM52361 standard; protein; 417 AA.
DE T26F17.15 protein.
PN FR2806095-A1.
PD 14-SEP-2001.
PA (GENT-) GENTECH SARL.
Query Match 14.3%; Score 66; DB 5; Length 417;
Best Local Similarity 23.8%; Pred. No. 55;
RESULT 335
ID ABB91091 standard; protein; 417 AA.
DE Herbicidically active polypeptide SEQ ID NO 302.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 14.3%; Score 66; DB 5; Length 417;
Best Local Similarity 23.8%; Pred. No. 55;
RESULT 336
ID AAR35445 standard; protein; 924 AA.
DE Human TPO lacking amino acids 713-721.
PN WO9303146-A1.
PD 18-FEB-1993.
PA (RAPO) RAPOPORT B.
Query Match 14.3%; Score 66; DB 2; Length 924;
Best Local Similarity 28.2%; Pred. No. 1.7e+02;
RESULT 337
ID AAR32875 standard; protein; 933 AA.
DE Human TPO.
PN WO9303146-A1.
PD 18-FEB-1993.
PA (RAPO) RAPOPORT B.
Query Match 14.3%; Score 66; DB 2; Length 933;
Best Local Similarity 28.2%; Pred. No. 1.7e+02;
RESULT 338
ID ADU68762 standard; protein; 933 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID568.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.

PA (BUCK-) BUCK INST AGE RES.
Query Match 14.3%; Score 66; DB 7; Length 933;
Best Local Similarity 28.2%; Pred. No. 1.7e+02;
RESULT 339
ID ADH88460 standard; protein; 247 AA.
DE Enterococcus faecalis polypeptide #2940.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC) DOUCETTE-STAMM L A.
PA (BUSH) BUSH D.
Query Match 14.2%; Score 65.5; DB 7; Length 247;
Best Local Similarity 30.8%; Pred. No. 30;
RESULT 340
ID ABJ19345 standard; protein; 778 AA.
DE NOVX related protein SEQ ID No 56.
PN WO200299062-A2.
PD 12-DEC-2002.
PA (CURA-) CURAGEN CORP.
Query Match 14.2%; Score 65.5; DB 6; Length 778;
Best Local Similarity 28.4%; Pred. No. 1.5e+02;
RESULT 341
ID ADO41690 standard; protein; 778 AA.
DE Novel human polypeptide NOV20b.
PN US2004018555-A1.
PD 29-JAN-2004.
PA (ANDE) ANDERSON D W.
PA (ZERH) ZERHUSEN B D.
PA (LILL) LI L.
PA (ZHON) ZHONG M.
PA (CASM) CASMAN S J.
PA (GERL) GERLACH V.
PA (SHIM) SHIMKETS R A.
PA (GORM) GORMAN L.
PA (PENA) PENA C E A.
PA (KEKU) KEKUDA R.
PA (PATT) PATTURAJAN M.
PA (SPYT) SPYTEK K A.
PA (LEIT) LEITE M W.
PA (RAST) RASTELLI L.
PA (MACD) MACDOUGALL J R.
PA (TAUP) TAUPIER R J.
PA (GUOX) GUO X S.
PA (MILL) MILLER C E.
PA (SHEN) SHENOY S G.
PA (HJAL) HJALT T.
PA (VOSS) VOSS E Z.
PA (BOLD) BOLDOG F L.
PA (MALY) MALYANKAR U M.
PA (PADI) PADIGARU M.
PA (JIWW) JI W.
PA (SMIT) SMITHSON G.
PA (EDIN) EDINGER S R.
PA (MILL) MILLET I.
PA (ELLE) ELLERMAN K.
Query Match 14.2%; Score 65.5; DB 8; Length 778;
Best Local Similarity 28.4%; Pred. No. 1.5e+02;
RESULT 342
ID ABU19344 standard; protein; 798 AA.
DE NOVX related protein SEQ ID No 54.
PN WO200299062-A2.
PD 12-DEC-2002.
PA (CURA-) CURAGEN CORP.
Query Match 14.2%; Score 65.5; DB 6; Length 798;
Best Local Similarity 28.4%; Pred. No. 1.6e+02;
RESULT 343
ID ADO41688 standard; protein; 798 AA.
DE Novel human polypeptide NOV20a.
PN US2004018555-A1.
PD 29-JAN-2004.
PA (ANDE) ANDERSON D W.
PA (ZERH) ZERHUSEN B D.
PA (LILL) LI L.
PA (ZHON) ZHONG M.

PA (CASM/) CASMAN S J.
PA (GERL/) GERLACH V.
PA (SHIM/) SHIMKETS R A.
PA (GORM/) GORMAN L.
PA (PENA/) PENNA C E A.
PA (KEKU/) KEKUDA R.
PA (PATT/) PATTAURAJAN M.
PA (SPVT/) SPYTEK K A.
PA (LEIT/) LEITE M W.
PA (RAST/) RASTELLI L.
PA (MACD/) MACDOUGALL J R.
PA (TAUP/) TAUPIER R J.
PA (GUOX/) GUO X S.
PA (MILL/) MILLER C E.
PA (SHEN/) SHENOV S G.
PA (HUAL/) HUALT T.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDOG F L.
PA (MALY/) MALYANKAR U M.
PA (PADI/) PADIGARU M.
PA (JIWW/) JI W.
PA (SMIT/) SMITHSON G.
PA (EDIN/) EDINGER S R.
PA (MILL/) MILLET I.
PA (ELLE/) ELLERMAN K.
Query Match 14.2%; Score 65.5; DB 8; Length 798;
Best Local Similarity 28.4%; Pred. No. 1.6e+02;
RESULT 344
ID ABP26174 standard; protein; 242 AA.
DE Streptococcus polypeptide SEQ ID NO 1524.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 14.1%; Score 65; DB 5; Length 242;
Best Local Similarity 28.1%; Pred. No. 34;
RESULT 345
ID AAG81855 standard; protein; 453 AA.
DE S. epidermidis open reading frame protein sequence SEQ ID NO:804.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 14.1%; Score 65; DB 3; Length 453;
Best Local Similarity 29.5%; Pred. No. 82;
RESULT 346
ID ABU42864 standard; protein; 453 AA.
DE Protein encoded by Prokaryotic essential gene #28391.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 14.1%; Score 65; DB 6; Length 453;
Best Local Similarity 29.5%; Pred. No. 82;
RESULT 347
ID ABF38759 standard; protein; 461 AA.
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3604.
PN USG380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 14.1%; Score 65; DB 5; Length 461;
Best Local Similarity 29.5%; Pred. No. 84;
RESULT 348
ID AAX35836 standard; protein; 126 AA.
DE Chlamydia pneumoniae lipoprotein sequence.
PN WO9927105-A2.
PD 03-JUN-1999.
PA (GEST) GENSET.
Query Match 13.9%; Score 64; DB 2; Length 126;
Best Local Similarity 24.8%; Pred. No. 18;
RESULT 349
ID ADM74713 standard; protein; 247 AA.
DE Fusarium oxysporum trypsinogen-like mutant protein - A226*.
PN WO200402920-A2.
PD 08-APR-2004.

PA (NOVO) NOVOZYMES BIOTECH INC.
Query Match 13.9%; Score 64; DB 8; Length 247;
Best Local Similarity 21.3%; Pred. No. 46;
RESULT 350
ID AAG57748 standard; protein; 249 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 74456.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 13.9%; Score 64; DB 3; Length 249;
Best Local Similarity 24.2%; Pred. No. 47;
RESULT 351
ID AAB24871 standard; peptide; 328 AA.
DE Plant SDF encoded polypeptide sequence SEQ List 1 NO:375.
PN WO200040695-A2.
PD 13-JUL-2000.
PA (CERE-) CERES INC.
Query Match 13.9%; Score 64; DB 3; Length 328;
Best Local Similarity 27.4%; Pred. No. 69;
RESULT 352
ID AAB24870 standard; peptide; 344 AA.
DE Plant SDF encoded polypeptide sequence SEQ List 1 NO:374.
PN WO200040695-A2.
PD 13-JUL-2000.
PA (CERE-) CERES INC.
Query Match 13.9%; Score 64; DB 3; Length 344;
Best Local Similarity 27.4%; Pred. No. 74;
RESULT 353
ID AAG04825 standard; protein; 414 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 998.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 13.9%; Score 64; DB 3; Length 414;
Best Local Similarity 24.2%; Pred. No. 96;
RESULT 354
ID AAG04824 standard; protein; 415 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 997.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 13.9%; Score 64; DB 3; Length 415;
Best Local Similarity 24.2%; Pred. No. 96;
RESULT 355
ID AAB24869 standard; peptide; 449 AA.
DE Plant SDF encoded polypeptide sequence SEQ List 1 NO:373.
PN WO200040695-A2.
PD 13-JUL-2000.
PA (CERE-) CERES INC.
Query Match 13.9%; Score 64; DB 3; Length 449;
Best Local Similarity 27.4%; Pred. No. 1.1e+02;
RESULT 356
ID ABP30895 standard; protein; 1550 AA.
DE Streptococcus polypeptide SEQ ID NO 10966.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 13.9%; Score 64; DB 5; Length 1550;
Best Local Similarity 36.8%; Pred. No. 6.1e+02;
RESULT 357
ID ABP29894 standard; protein; 1570 AA.
DE Streptococcus polypeptide SEQ ID NO 8964.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 13.9%; Score 64; DB 5; Length 1570;
Best Local Similarity 36.8%; Pred. No. 6.2e+02;
RESULT 358
ID ABP30531 standard; protein; 1570 AA.
DE Streptococcus polypeptide SEQ ID NO 10238.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.

Query Match 13.9%; Score 64; DB 5; Length 1570;
 Best Local Similarity 36.8%; Pred. No. 6.2e+02;
 RESULT 359
 ID ABP28560 standard; protein; 1590 AA.
 DE Streptococcus polypeptide SEQ ID NO 6296.
 PN WO200234771-A2.
 PD 02-MAY-2002.
 PA (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 Query Match 13.9%; Score 64; DB 5; Length 1590;
 Best Local Similarity 36.8%; Pred. No. 6.3e+02;
 RESULT 360
 ID ADD01197 standard; protein; 1675 AA.
 DE Human nucleic acid-associated protein NAAP-35 SEQ ID NO:35.
 PN WO2003054219-A2.
 PD 03-JUL-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 13.9%; Score 64; DB 7; Length 1675;
 Best Local Similarity 30.0%; Pred. No. 6.8e+02;
 RESULT 361
 ID ABG22718 standard; protein; 1685 AA.
 DE Novel human diagnostic protein #22709.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 13.9%; Score 64; DB 4; Length 1685;
 Best Local Similarity 30.0%; Pred. No. 6.9e+02;
 RESULT 362
 ID AAE22840 standard; protein; 183 AA.
 DE Human phospholipase A2-like enzyme #2.
 PN WO200231162-A2.
 PD 18-APR-2002.
 PA (FARB) BAYER AG.
 Query Match 13.7%; Score 63.5; DB 5; Length 183;
 Best Local Similarity 27.1%; Pred. No. 35;
 RESULT 363
 ID ABB60434 standard; protein; 216 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 8094.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PKPE) PE CORP NY.
 Query Match 13.7%; Score 63.5; DB 4; Length 216;
 Best Local Similarity 29.2%; Pred. No. 44;
 RESULT 364
 ID ADB46124 standard; protein; 317 AA.
 DE Bread wheat thiamine biosynthetic enzyme 1 polypeptide #5.
 PN US6512164-B1.
 PD 28-JAN-2003.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 Query Match 13.7%; Score 63.5; DB 7; Length 317;
 Best Local Similarity 24.2%; Pred. No. 76;
 RESULT 365
 ID AAM14478 standard; protein; 575 AA.
 DE Peptide #912 encoded by probe for measuring cervical gene expression.
 PN WO200157278-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 13.7%; Score 63.5; DB 4; Length 575;
 Best Local Similarity 42.6%; Pred. No. 1.7e+02;
 RESULT 366
 ID ABB33426 standard; peptide; 575 AA.
 DE Peptide #932 encoded by human foetal liver single exon probe.
 PN WO200157277-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 13.7%; Score 63.5; DB 4; Length 575;
 Best Local Similarity 42.6%; Pred. No. 1.7e+02;
 RESULT 367
 ID AAM26891 standard; protein; 575 AA.
 DE Peptide #928 encoded by probe for measuring placental gene expression.
 PN WO200157272-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match 13.7%; Score 63.5; DB 4; Length 575;
 Best Local Similarity 42.6%; Pred. No. 1.7e+02;
 RESULT 368
 ID ABB28251 standard; peptide; 575 AA.
 DE Human peptide #902 encoded by breast cell single exon nucleic acid probe.
 PN WO200157271-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 13.7%; Score 63.5; DB 4; Length 575;
 Best Local Similarity 42.6%; Pred. No. 1.7e+02;
 RESULT 369
 ID ABB18885 standard; protein; 575 AA.
 DE Protein #884 encoded by probe for measuring heart cell gene expression.
 PN WO200157274-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 13.7%; Score 63.5; DB 4; Length 575;
 Best Local Similarity 42.6%; Pred. No. 1.7e+02;
 RESULT 370
 ID AAM66605 standard; protein; 575 AA.
 DE Human bone marrow expressed probe encoded protein SEQ ID NO: 26911.
 PN WO200157276-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 13.7%; Score 63.5; DB 4; Length 575;
 Best Local Similarity 42.6%; Pred. No. 1.7e+02;
 RESULT 371
 ID AAM54211 standard; protein; 575 AA.
 DE Human brain expressed single exon probe encoded protein SEQ ID NO: 26316.
 PN WO200157275-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 13.7%; Score 63.5; DB 4; Length 575;
 Best Local Similarity 42.6%; Pred. No. 1.7e+02;
 RESULT 372
 ID ABG48273 standard; peptide; 575 AA.
 DE Human liver peptide, SEQ ID No 26921.
 PN WO200157273-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 13.7%; Score 63.5; DB 4; Length 575;
 Best Local Similarity 42.6%; Pred. No. 1.7e+02;
 RESULT 373
 ID AAM22205 standard; protein; 575 AA.
 DE Peptide #887 encoded by probe for measuring human breast gene expression.
 PN WO200157270-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 13.7%; Score 63.5; DB 4; Length 575;
 Best Local Similarity 42.6%; Pred. No. 1.7e+02;
 RESULT 374
 ID ABG36257 standard; peptide; 575 AA.
 DE Human peptide encoded by genome-derived single exon probe SEQ ID 25922.
 PN WO200186003-A2.
 PD 15-NOV-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 13.7%; Score 63.5; DB 5; Length 575;
 Best Local Similarity 42.6%; Pred. No. 1.7e+02;
 RESULT 375
 ID ADH72316 standard; protein; 596 AA.
 DE Human protein of the invention NOV62f SEQ ID NO:1212.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 13.7%; Score 63.5; DB 8; Length 596;
 Best Local Similarity 42.6%; Pred. No. 1.8e+02;
 RESULT 376
 ID ADD18216 standard; protein; 600 AA.
 DE Human molecule (MOL) protein MOL2b.
 PN WO2003003984-A2.
 PD 16-JAN-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 13.7%; Score 63.5; DB 7; Length 600;

Best Local Similarity 42.6%; Pred. No. 1.9e+02;
RESULT 377
ID ADL18218 standard; protein; 600 AA.
DE Human molecule (MOL) protein MOL2c.
PN WO200303984-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 13.7%; Score 63.5; DB 7; Length 600;
Best Local Similarity 42.6%; Pred. No. 1.9e+02;
RESULT 378
ID ADH72308 standard; protein; 600 AA.
DE Human protein of the invention NOV62b SEQ ID NO:1204.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 13.7%; Score 63.5; DB 8; Length 600;
Best Local Similarity 42.6%; Pred. No. 1.9e+02;
RESULT 379
ID ADH72310 standard; protein; 600 AA.
DE Human protein of the invention NOV62c SEQ ID NO:1206.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 13.7%; Score 63.5; DB 8; Length 600;
Best Local Similarity 42.6%; Pred. No. 1.9e+02;
RESULT 380
ID ABP51377 standard; protein; 646 AA.
DE Human MDDT SEQ ID NO 399.
PN WO200240715-A2.
PD 23-MAY-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 13.7%; Score 63.5; DB 5; Length 646;
Best Local Similarity 24.3%; Pred. No. 2.1e+02;
RESULT 381
ID ADN73817 standard; protein; 651 AA.
DE Thale cress protein repressed in E2Fa/Dpa expressing plants SeqID 1712.
PN WO200403798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDESIGN NV.
Query Match 13.7%; Score 63.5; DB 8; Length 651;
Best Local Similarity 39.0%; Pred. No. 2.1e+02;
RESULT 382
ID ADP76731 standard; protein; 669 AA.
DE Novel human secreted and transmembrane protein SeqID 406.
PN WO2003072035-A2.
PD 04-SEP-2003.
PA (GETH-) GENENTECH INC.
Query Match 13.7%; Score 63.5; DB 7; Length 669;
Best Local Similarity 23.5%; Pred. No. 2.2e+02;
RESULT 383
ID ADQ20963 standard; protein; 669 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 3783.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 13.7%; Score 63.5; DB 8; Length 669;
Best Local Similarity 23.5%; Pred. No. 2.2e+02;
RESULT 384
ID ADB4653 standard; protein; 742 AA.
DE Human protein encoded by clone MESAN20021220.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 13.7%; Score 63.5; DB 7; Length 742;
Best Local Similarity 42.6%; Pred. No. 2.5e+02;
RESULT 385
ID ADE31223 standard; protein; 753 AA.
DE Human diagnostic and therapeutic polypeptide (DITHP), SEQ ID No 355.
PN WO2003062376-A2.
PD 31-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 13.7%; Score 63.5; DB 7; Length 753;
Best Local Similarity 42.6%; Pred. No. 2.6e+02;
RESULT 386
ID ABU31950 standard; protein; 762 AA.
DE Protein encoded by prokaryotic essential gene #17477.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 13.7%; Score 63.5; DB 6; Length 762;
Best Local Similarity 29.9%; Pred. No. 2.6e+02;
RESULT 387
ID AAE22843 standard; protein; 802 AA.
DE Human phospholipase A2-like enzyme #5.
PN WO200231162-A2.
PD 18-APR-2002.
PA (FARB-) BAYER AG.
Query Match 13.7%; Score 63.5; DB 5; Length 802;
Best Local Similarity 27.1%; Pred. No. 2.8e+02;
RESULT 388
ID ADB61634 standard; protein; 818 AA.
DE Human 818 amino acid phospholipase A2 (PLA2) protein.
PN WO2003060132-A1.
PD 24-JUL-2003.
PA (TANA-) TANABE SEIYAKU CO.
Query Match 13.7%; Score 63.5; DB 7; Length 818;
Best Local Similarity 27.1%; Pred. No. 2.9e+02;
RESULT 389
ID ADH72314 standard; protein; 819 AA.
DE Human protein of the invention NOV62e SEQ ID NO:1210.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 13.7%; Score 63.5; DB 8; Length 819;
Best Local Similarity 42.6%; Pred. No. 2.9e+02;
RESULT 390
ID ABU01959 standard; protein; 832 AA.
DE Human IGFALS similar protein SEQ ID No 660.
PN WO200216593-A2.
PD 28-FEB-2002.
PA (AGEN-) AGENSYS INC.
Query Match 13.7%; Score 63.5; DB 5; Length 832;
Best Local Similarity 42.6%; Pred. No. 2.9e+02;
RESULT 391
ID AAE22221 standard; protein; 837 AA.
DE Human toll like receptor like molecule 4 (TLR-L4) protein.
PN WO200220569-A2.
PD 14-MAR-2002.
PA (SCHE-) SCHERING CORP.
Query Match 13.7%; Score 63.5; DB 5; Length 837;
Best Local Similarity 42.6%; Pred. No. 3e+02;
RESULT 392
ID ADF69111 standard; protein; 853 AA.
DE Human WF53 protein sequence SEQ ID NO:81.
PN WO2003083047-A2.
PD 09-OCT-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 13.7%; Score 63.5; DB 7; Length 853;
Best Local Similarity 42.6%; Pred. No. 3e+02;
RESULT 393
ID AAG67510 standard; protein; 866 AA.
DE Amino acid sequence of a human secreted polypeptide.
PN WO200166690-A2.
PD 13-SEP-2001.
PA (SMIK-) SMITHKLINE BEECHAM CORP.
PA (SMIK-) SMITHKLINE BEECHAM PLC.
Query Match 13.7%; Score 63.5; DB 4; Length 866;
Best Local Similarity 42.6%; Pred. No. 3.1e+02;
RESULT 394
ID AAE18209 standard; protein; 876 AA.
DE Human MOL2 protein.
PN WO200206339-A2.
PD 24-JAN-2002.
PA (CURA-) CURAGEN CORP.
Query Match 13.7%; Score 63.5; DB 5; Length 876;

Best Local Similarity 42.6%; Pred. No. 3.2e+02;
RESULT 395
ID AD18196 standard; protein; 876 AA.
DE Human molecule (MOL) protein MOL2a.
PN WO2003003984-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 13.7%; Score 63.5; DB 7; Length 876;
Best Local Similarity 42.6%; Pred. No. 3.2e+02;
RESULT 396
ID ADH72306 standard; protein; 876 AA.
DE Human protein of the invention NOV62a SEQ ID NO:1202.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 13.7%; Score 63.5; DB 8; Length 876;
Best Local Similarity 42.6%; Pred. No. 3.2e+02;
RESULT 397
ID ADH72312 standard; protein; 876 AA.
DE Human protein of the invention NOV62d SEQ ID NO:1208.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 13.7%; Score 63.5; DB 8; Length 876;
Best Local Similarity 42.6%; Pred. No. 3.2e+02;
RESULT 398
ID ABO65486 standard; protein; 881 AA.
DE Klebsiella pneumoniae polypeptide seqid 12003.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 13.7%; Score 63.5; DB 7; Length 881;
Best Local Similarity 29.9%; Pred. No. 3.2e+02;
RESULT 399
ID ADK64936 standard; protein; 882 AA.
DE Disease treating protein complex-derived protein #1548.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 13.7%; Score 63.5; DB 7; Length 882;
Best Local Similarity 20.8%; Pred. No. 3.2e+02;
RESULT 400
ID ABB07497 standard; protein; 1026 AA.
DE Human lipid metabolism molecule (LMM) polypeptide (ID: 7477093CD1).
PN WO200204490-A2.
PD 17-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 13.7%; Score 63.5; DB 5; Length 1026;
Best Local Similarity 27.1%; Pred. No. 3.9e+02;
RESULT 401
ID ADC10174 standard; protein; 1045 AA.
DE Human NOVX polypeptide SEQ ID NO: 196.
PN WO2003000842-A2.
PD 03-JAN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 13.7%; Score 63.5; DB 7; Length 1045;
Best Local Similarity 27.1%; Pred. No. 4e+02;
RESULT 402
ID ABP78966 standard; protein; 107 AA.
DE N. gonorrhoeae amino acid sequence SEQ ID 4462.
PN WO200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Query Match 13.6%; Score 63; DB 6; Length 107;
Best Local Similarity 25.6%; Pred. No. 19;
RESULT 403
ID AAG82718 standard; protein; 186 AA.
DE S. epidermidis open reading frame protein sequence SEQ ID NO:2530.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 13.6%; Score 63; DB 4; Length 186;
Best Local Similarity 28.6%; Pred. No. 41;
RESULT 404
ID ABP39410 standard; protein; 315 AA.
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4255.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 13.6%; Score 63; DB 5; Length 315;
Best Local Similarity 28.6%; Pred. No. 87;
RESULT 405
ID AAG61478 standard; protein; 414 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 79745.
PN EP1033405-A2.
PD 06-SRP-2000.
Query Match 13.6%; Score 63; DB 3; Length 414;
Best Local Similarity 24.2%; Pred. No. 1.3e+02;
RESULT 406
ID AAG61477 standard; protein; 415 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 79744.
PN EP1033405-A2.
PD 06-SRP-2000.
Query Match 13.6%; Score 63; DB 3; Length 415;
Best Local Similarity 24.2%; Pred. No. 1.3e+02;
RESULT 407
ID AAY40501 standard; protein; 441 AA.
DE A. thaliana yael polypeptide.
PN WO9947553-A2.
PD 23-SEP-1999.
PA (GLAX) GLAXO GROUP LTD.
Query Match 13.6%; Score 63; DB 2; Length 441;
Best Local Similarity 23.1%; Pred. No. 1.4e+02;
RESULT 408
ID ADB65212 standard; protein; 592 AA.
DE Human protein encoded by clone TEST110001570.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
Query Match 13.6%; Score 63; DB 7; Length 592;
Best Local Similarity 30.5%; Pred. No. 2.1e+02;
RESULT 409
ID ADA54600 standard; protein; 295 AA.
DE Human protein, SEQ ID 2168.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
Query Match 13.5%; Score 62.5; DB 6; Length 295;
Best Local Similarity 33.3%; Pred. No. 91;
RESULT 410
ID ADJ70687 standard; protein; 295 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID2493.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
Query Match 13.5%; Score 62.5; DB 7; Length 295;
Best Local Similarity 33.3%; Pred. No. 91;
RESULT 411
ID ABE77902 standard; protein; 379 AA.
DE High level promoter polypeptide #6.
PN WO200261098-A2.
PD 08-AUG-2002.
PA (DUPO-) DU PONT DE NEMOURS & CO E I.
Query Match 13.5%; Score 62.5; DB 5; Length 379;
Best Local Similarity 26.5%; Pred. No. 1.3e+02;
RESULT 412
ID ABB58263 standard; protein; 404 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 1581.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 13.5%; Score 62.5; DB 4; Length 404;
Best Local Similarity 27.0%; Pred. No. 1.4e+02;

RESULT 413
ID AAU16300 standard; protein; 264 AA.
DE Human novel secreted protein, Seq ID 1253.
PN WO20015322-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.4%; Score 62; DB 4; Length 264;
Best Local Similarity 30.4%; Pred. No. 90;
RESULT 414
ID ABUS5369 standard; protein; 264 AA.
DE Human novel polypeptide #456.
PN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 13.4%; Score 62; DB 6; Length 264;
Best Local Similarity 30.4%; Pred. No. 90;
RESULT 415
ID AAY79170 standard; protein; 1017 AA.
DE Pneumocystis carinii major surface glycoprotein HMSG33.
PN WO200009760-A1.
PD 24-FEB-2000.
PA (USHS) US DEPT HEALTH & HUMAN SERVICES.
Query Match 13.4%; Score 62; DB 3; Length 1017;
Best Local Similarity 28.9%; Pred. No. 6e+02;
RESULT 416
ID AAY79171 standard; protein; 1023 AA.
DE Pneumocystis carinii major surface glycoprotein HMSG35.
PN WO200009760-A1.
PD 24-FEB-2000.
PA (USHS) US DEPT HEALTH & HUMAN SERVICES.
Query Match 13.4%; Score 62; DB 3; Length 1023;
Best Local Similarity 28.9%; Pred. No. 6e+02;
RESULT 417
ID AAY79168 standard; protein; 1027 AA.
DE Pneumocystis carinii major surface glycoprotein HMSG14.
PN WO200009760-A1.
PD 24-FEB-2000.
PA (USHS) US DEPT HEALTH & HUMAN SERVICES.
Query Match 13.4%; Score 62; DB 3; Length 1027;
Best Local Similarity 28.9%; Pred. No. 6e+02;
RESULT 418
ID AAY51652 standard; protein; 1634 AA.
DE M. jannaschii MJ0885 protein fragment.
PN WO200008164-A2.
PD 17-FEB-2000.
PA (LION-) LION BIOSCIENCE AG.
Query Match 13.4%; Score 62; DB 3; Length 1634;
Best Local Similarity 29.2%; Pred. No. 1.2e+03;
RESULT 419
ID AAY52023 standard; protein; 1634 AA.
DE M. jannaschii MJ0885 protein.
PN DE19840771-A1.
PD 10-FEB-2000.
PA (LION-) LION BIOSCIENCE AG.
Query Match 13.4%; Score 62; DB 3; Length 1634;
Best Local Similarity 29.2%; Pred. No. 1.2e+03;
RESULT 420
ID ADN59962 standard; protein; 1634 AA.
DE Methanococcus jannaschii DNA polymerase protein SEQ ID NO:23.
PN WO2000403947-A2.
PD 13-MAY-2004.
PA (STRA-) STRATAGENE.
Query Match 13.4%; Score 62; DB 8; Length 1634;
Best Local Similarity 29.2%; Pred. No. 1.2e+03;
RESULT 421
ID ABB61677 standard; protein; 2075 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 11823.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 13.4%; Score 62; DB 4; Length 2075;
Best Local Similarity 29.2%; Pred. No. 1.2e+03;
RESULT 422
ID AAY11878 standard; protein; 109 AA.
DE Human S' EST secreted protein SEQ ID No: 478.
PN WO9906550-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 13.3%; Score 61.5; DB 2; Length 109;
Best Local Similarity 28.6%; Pred. No. 30;
RESULT 423
ID ADO16891 standard; protein; 142 AA.
DE Tobacco budworm voltage gated calcium channel subunit protein SeqID 4.
PN WO200404553-A2.
PD 27-MAY-2004.
PA (FMCC) FMC CORP.
Query Match 13.3%; Score 61.5; DB 8; Length 142;
Best Local Similarity 36.2%; Pred. No. 43;
RESULT 424
ID ABP65799 standard; protein; 566 AA.
DE Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:543.
PN EP1227152-A1.
PD 31-JUL-2002.
PA (NEST) SOC PROD NESTLE SA.
Query Match 13.3%; Score 61.5; DB 5; Length 566;
Best Local Similarity 31.5%; Pred. No. 3e+02;
RESULT 425
ID ABB58375 standard; protein; 581 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 1917.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 13.3%; Score 61.5; DB 4; Length 581;
Best Local Similarity 27.5%; Pred. No. 3.1e+02;
RESULT 426
ID ADJ50375 standard; protein; 602 AA.
DE Oil-associated gene related protein #1875.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match 13.3%; Score 61.5; DB 8; Length 602;
Best Local Similarity 26.7%; Pred. No. 3.3e+02;
RESULT 427
ID ABB91263 standard; protein; 626 AA.
DE Herbicidically active polypeptide SEQ ID NO 474.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 13.3%; Score 61.5; DB 5; Length 626;
Best Local Similarity 26.7%; Pred. No. 3.5e+02;
RESULT 428
ID ADJ49225 standard; protein; 626 AA.
DE Oil-associated gene related protein #725.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match 13.3%; Score 61.5; DB 8; Length 626;
Best Local Similarity 26.7%; Pred. No. 3.5e+02;
RESULT 429
ID ADJ49944 standard; protein; 668 AA.
DE Oil-associated gene related protein #1444.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.

PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match 13.3%; Score 61.5; DB 8; Length 668;
Best Local Similarity 26.7%; Pred. No. 3.8e+02;
RESULT 430
ID AAM60216 standard; protein; 789 AA.
DE Bacillus thuringiensis insecticidal 81F toxin.
PN WO9818932-A2.
PD 07-MAY-1998.
PA (MYCO) MYCOGEN CORP.
Query Match 13.3%; Score 61.5; DB 2; Length 789;
Best Local Similarity 41.2%; Pred. No. 4.8e+02;
RESULT 431
ID AAW46866 standard; protein; 789 AA.
DE Bacillus thuringiensis toxin designated 185U2(a).
PN WO9800546-A2.
PD 08-JAN-1998.
PA (MYCO) MYCOGEN CORP.
Query Match 13.3%; Score 61.5; DB 2; Length 789;
Best Local Similarity 41.2%; Pred. No. 4.8e+02;
RESULT 432
ID AAY24969 standard; protein; 789 AA.
DE Bacillus thuringiensis toxin 185U2(a).
PN WO9933991-A2.
PD 08-JUL-1999.
PA (MYCO) MYCOGEN CORP.
Query Match 13.3%; Score 61.5; DB 2; Length 789;
Best Local Similarity 41.2%; Pred. No. 4.8e+02;
RESULT 433
ID ADO16893 standard; protein; 1764 AA.
DE Tobacco budworm voltage gated calcium channel subunit protein seqID 6.
PN WO2004044553-A2.
PD 27-MAY-2004.
PA (FWCC) FWC CORP.
Query Match 13.3%; Score 61.5; DB 2; Length 789;
Best Local Similarity 41.2%; Pred. No. 4.8e+02;
RESULT 434
ID AAR22360 standard; protein; 237 AA.
DE CO-029 tumour associated antigen protein.
PN EP478146-A.
PD 01-APR-1992.
PA (WIST-) WISTAR INST.
Query Match 13.2%; Score 61; DB 2; Length 237;
Best Local Similarity 26.6%; Pred. No. 1e+02;
RESULT 435
ID AAM24510 standard; protein; 237 AA.
DE C884P predicted amino acid sequence.
PN WO200149716-A2.
PD 12-JUL-2001.
PA (CORI-) CORIXA CORP.
Query Match 13.2%; Score 61; DB 4; Length 237;
Best Local Similarity 26.6%; Pred. No. 1e+02;
RESULT 436
ID ABP55359 standard; protein; 237 AA.
DE Human colon tumour protein for clone C884P SEQ ID NO:1062.
PN WO200283070-A2.
PD 24-OCT-2002.
PA (CORI-) CORIXA CORP.
Query Match 13.2%; Score 61; DB 6; Length 237;
Best Local Similarity 26.6%; Pred. No. 1e+02;
RESULT 437
ID ADD4677 standard; protein; 237 AA.
DE Human protein P19075, SEQ ID NO 10308.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 13.2%; Score 61; DB 7; Length 237;
Best Local Similarity 26.6%; Pred. No. 1e+02;
RESULT 438
ID ADN39984 standard; protein; 237 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C354.
PN WO2003042661-A2.

PD 22-MAY-2003.
PA (BOSB-) BOS BIOTECHNOLOGY INC.
Query Match 13.2%; Score 61; DB 7; Length 237;
Best Local Similarity 26.6%; Pred. No. 1e+02;
RESULT 439
ID ADL12487 standard; protein; 237 AA.
DE Human steroid-induced C3A liver cell protein #30.
PN US6673549-B1.
PD 06-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match 13.2%; Score 61; DB 8; Length 237;
Best Local Similarity 26.6%; Pred. No. 1e+02;
RESULT 440
ID ADN04002 standard; protein; 237 AA.
DE Antipsoriatic protein sequence #196.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 13.2%; Score 61; DB 8; Length 237;
Best Local Similarity 26.6%; Pred. No. 1e+02;
RESULT 441
ID AAB43590 standard; protein; 241 AA.
DE Human cancer associated protein sequence SEQ ID NO:1035.
PN WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.2%; Score 61; DB 3; Length 241;
Best Local Similarity 26.6%; Pred. No. 1e+02;
RESULT 442
ID AAG74331 standard; protein; 241 AA.
DE Human colon cancer antigen protein SEQ ID NO:5095.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.2%; Score 61; DB 4; Length 241;
Best Local Similarity 26.6%; Pred. No. 1e+02;
RESULT 443
ID ABP55387 standard; protein; 243 AA.
DE Human colon tumour related protein sequence SEQ ID NO:1122.
PN WO200283070-A2.
PD 24-OCT-2002.
PA (CORI-) CORIXA CORP.
Query Match 13.2%; Score 61; DB 6; Length 243;
Best Local Similarity 26.6%; Pred. No. 1.1e+02;
RESULT 444
ID ABO72546 standard; protein; 254 AA.
DE Pseudomonas aeruginosa polypeptide #4721.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 13.2%; Score 61; DB 7; Length 254;
Best Local Similarity 28.8%; Pred. No. 1.1e+02;
RESULT 445
ID AAG12819 standard; protein; 306 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 12078.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 13.2%; Score 61; DB 3; Length 306;
Best Local Similarity 26.0%; Pred. No. 1.5e+02;
RESULT 446
ID AAG12818 standard; protein; 312 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 12077.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 13.2%; Score 61; DB 3; Length 312;
Best Local Similarity 26.0%; Pred. No. 1.5e+02;
RESULT 447
ID ABP55373 standard; protein; 344 AA.
DE Human colon tumour protein for Ral2-C884P SEQ ID NO:1085.
PN WO200283070-A2.
PD 24-OCT-2002.
PA (CORI-) CORIXA CORP.
Query Match 13.2%; Score 61; DB 6; Length 344;

Best Local Similarity 26.6%; Pred. No. 1.7e+02;
RESULT 448
ID ABP55386 standard; protein; 446 AA.
DE Human colon tumour related protein sequence SEQ ID NO:1121.
PN WO200283070-A2.
PD 24-OCT-2002.
PA (CORI-) CORIXA CORP.
Query Match 13.2%; Score 61; DB 6; Length 446;
Best Local Similarity 26.6%; Pred. No. 2.5e+02;
RESULT 449
ID ABP35647 standard; protein; 790 AA.
DE Fungal ZBC protein sequence #73.
PN WO200224865-A2.
PD 28-MAR-2002.
PA (NICR-) MICROBIA INC.
Query Match 13.2%; Score 61; DB 5; Length 790;
Best Local Similarity 35.3%; Pred. No. 5.5e+02;
RESULT 450
ID AAB40536 standard; protein; 111 AA.
DE Human ORFX ORF300 polypeptide sequence SEQ ID NO:600.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 13.1%; Score 60.5; DB 3; Length 111;
Best Local Similarity 30.1%; Pred. No. 41;
RESULT 451
ID ABP08727 standard; protein; 111 AA.
DE Human ORFX protein sequence SEQ ID NO:17436.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match 13.1%; Score 60.5; DB 5; Length 111;
Best Local Similarity 30.1%; Pred. No. 41;
RESULT 452
ID AAG00151 standard; protein; 118 AA.
DE Human secreted protein, SEQ ID NO: 4232.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 13.1%; Score 60.5; DB 3; Length 118;
Best Local Similarity 32.7%; Pred. No. 44;
RESULT 453
ID ABM65002 standard; protein; 135 AA.
DE Propionibacterium acnes immunogenic polypeptide #29678.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 13.1%; Score 60.5; DB 6; Length 135;
Best Local Similarity 25.7%; Pred. No. 54;
RESULT 454
ID AAW98230 standard; protein; 221 AA.
DE H. pylori GHPO 1578 protein.
PN WO9843478-A1.
PD 08-OCT-1998.
PA (INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.1%; Score 60.5; DB 2; Length 221;
Best Local Similarity 27.3%; Pred. No. 1.1e+02;
RESULT 455
ID ABG19614 standard; protein; 245 AA.
DE Novel human diagnostic protein #19605.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.1%; Score 60.5; DB 4; Length 245;
Best Local Similarity 26.7%; Pred. No. 1.2e+02;
RESULT 456
ID AAU37300 standard; protein; 262 AA.
DE Staphylococcus aureus cellular proliferation protein #1470.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 13.1%; Score 60.5; DB 4; Length 262;

Best Local Similarity 23.9%; Pred. No. 1.4e+02;
RESULT 457
ID AAU34364 standard; protein; 262 AA.
DE Staphylococcus aureus cellular proliferation protein #640.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 13.1%; Score 60.5; DB 4; Length 262;
Best Local Similarity 23.9%; Pred. No. 1.4e+02;
RESULT 458
ID ABU43976 standard; protein; 464 AA.
DE Protein encoded by Prokaryotic essential gene #29503.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 13.1%; Score 60.5; DB 6; Length 464;
Best Local Similarity 18.8%; Pred. No. 3e+02;
RESULT 459
ID ABG26239 standard; protein; 467 AA.
DE Novel human diagnostic protein #26230.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.1%; Score 60.5; DB 4; Length 467;
Best Local Similarity 26.7%; Pred. No. 3.1e+02;
RESULT 460
ID ADE56988 standard; protein; 567 AA.
DE Rat Protein P38439, SEQ ID NO 2843.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 13.1%; Score 60.5; DB 7; Length 567;
Best Local Similarity 28.1%; Pred. No. 4e+02;
RESULT 461
ID AAP93971 standard; protein; 647 AA.
DE Human carbasstatin-like polypeptide.
PN JP01283300-A.
PD 14-NOV-1989.
PA (TAKI) TAKARA SHUZO CO LTD.
Query Match 13.1%; Score 60.5; DB 1; Length 647;
Best Local Similarity 26.7%; Pred. No. 4.8e+02;
RESULT 462
ID ABP35619 standard; protein; 654 AA.
DE Fungal ZBC protein sequence #45.
PN WO200224865-A2.
PD 28-MAR-2002.
PA (MICR-) MICROBIA INC.
Query Match 13.1%; Score 60.5; DB 5; Length 654;
Best Local Similarity 34.4%; Pred. No. 4.9e+02;
RESULT 463
ID ABG93214 standard; protein; 676 AA.
DE S. cerevisiae BAX-associated protein fragment SEQ ID 386.
PN WO200264766-A2.
PD 22-AUG-2002.
PA (JANC) JANSSEN PHARM NV.
Query Match 13.1%; Score 60.5; DB 5; Length 676;
Best Local Similarity 29.3%; Pred. No. 5.1e+02;
RESULT 464
ID AAR85596 standard; protein; 694 AA.
DE Human calpastatin.
PN WO9533060-A1.
PD 07-DEC-1995.
PA (RHON) RHONE-POULENC ROBER SA.
Query Match 13.1%; Score 60.5; DB 2; Length 694;
Best Local Similarity 26.7%; Pred. No. 5.3e+02;
RESULT 465
ID ABR58343 standard; protein; 708 AA.
DE BAA03747 protein #SEQ ID 112.
PN WO2003029421-A2.
PD 10-APR-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 13.1%; Score 60.5; DB 6; Length 708;


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Best Local Similarity 26.7%; Pred. No. 5.5e+02;
RESULT 466
ID ADE63695 standard; protein; 708 AA.
DE Human Protein P20810, SEQ ID NO 9639.
PN W02003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 13.1%; Score 60.5; DB 7; Length 708;
Best Local Similarity 26.7%; Pred. No. 5.5e+02;
RESULT 467
ID ADD44901 standard; protein; 708 AA.
DE Human Protein XP_051211, SEQ ID NO 10332.
PN W02003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 13.1%; Score 60.5; DB 7; Length 708;
Best Local Similarity 26.7%; Pred. No. 5.5e+02;
RESULT 468
ID ADD4905 standard; protein; 708 AA.
DE Human Protein XP_051211, SEQ ID NO 10336.
PN W02003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 13.1%; Score 60.5; DB 7; Length 708;
Best Local Similarity 26.7%; Pred. No. 5.5e+02;
RESULT 469
ID ADE63699 standard; protein; 708 AA.
DE Human Protein P20810, SEQ ID NO 9643.
PN W02003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 13.1%; Score 60.5; DB 7; Length 708;
Best Local Similarity 26.7%; Pred. No. 5.5e+02;
RESULT 470
ID ADE61234 standard; protein; 708 AA.
DE Human protein tyrosine kinase biomarker calpastatin protein.
PN W02004020583-A2.
PD 11-MAR-2004.
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
Query Match 13.1%; Score 60.5; DB 8; Length 708;
Best Local Similarity 26.7%; Pred. No. 5.5e+02;
RESULT 471
ID ABR58316 standard; protein; 750 AA.
DE BC0715C protein #SEQ ID 78.
PN W02003029421-A2.
PD 10-APR-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 13.1%; Score 60.5; DB 6; Length 750;
Best Local Similarity 26.7%; Pred. No. 5.9e+02;
RESULT 472
ID AAY70008 standard; protein; 754 AA.
DE Human protease and associated protein-2 (PRG-2).
PN W0200009709-A2.
PD 24-FEB-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 13.1%; Score 60.5; DB 3; Length 754;
Best Local Similarity 26.7%; Pred. No. 6e+02;
RESULT 473
ID ABR58315 standard; protein; 769 AA.
DE BC00715B protein #SEQ ID 76.
PN W02003029421-A2.
PD 10-APR-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 13.1%; Score 60.5; DB 6; Length 769;
Best Local Similarity 26.7%; Pred. No. 6.1e+02;
RESULT 474
ID ABR58314 standard; protein; 791 AA.
DE BC00715A protein #SEQ ID 74.
PN W02003029421-A2.
PD 28-NOV-2002.
PD 10-APR-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 13.1%; Score 60.5; DB 4; Length 791;
Best Local Similarity 26.7%; Pred. No. 6.4e+02;
RESULT 475
ID AAB95467 standard; protein; 874 AA.
DE Human protein sequence SEQ ID NO:17957.
PN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 13.1%; Score 60.5; DB 4; Length 874;
Best Local Similarity 21.6%; Pred. No. 7.4e+02;
RESULT 476
ID ABG26235 standard; protein; 1054 AA.
DE Novel human diagnostic protein #26226.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.1%; Score 60.5; DB 4; Length 1054;
Best Local Similarity 26.7%; Pred. No. 9.6e+02;
RESULT 477
ID AAU14626 standard; protein; 1150 AA.
DE Novel bone marrow polypeptide #25.
PN W0200157187-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.1%; Score 60.5; DB 4; Length 1150;
Best Local Similarity 43.6%; Pred. No. 1.1e+03;
RESULT 478
ID ABB68731 standard; protein; 1264 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 32985.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 13.1%; Score 60.5; DB 4; Length 1264;
Best Local Similarity 27.3%; Pred. No. 1.2e+03;
RESULT 479
ID ABB80241 standard; protein; 1571 AA.
DE CspA.
PN W02003059252-A2.
PD 24-JUL-2003.
PA (CHIL-) CHILDREN'S HOSPITAL & REGIONAL MEDICAL.
Query Match 13.1%; Score 60.5; DB 7; Length 1571;
Best Local Similarity 40.7%; Pred. No. 1.7e+03;
RESULT 480
ID ABP71293 standard; protein; 1579 AA.
DE Group B Streptococcus BVH-A5 polypeptide.
PN W02003004650-A2.
PD 16-JAN-2003.
PA (SHIR-) SHIRE BIOCHEM INC.
Query Match 13.1%; Score 60.5; DB 6; Length 1579;
Best Local Similarity 40.7%; Pred. No. 1.7e+03;
RESULT 481
ID AAU14794 standard; protein; 2298 AA.
DE Novel bone marrow polypeptide #193.
PN W0200157187-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.1%; Score 60.5; DB 4; Length 2298;
Best Local Similarity 43.6%; Pred. No. 2.9e+03;
RESULT 482
ID AAU14720 standard; protein; 2301 AA.
DE Novel bone marrow polypeptide #119.
PN W0200157187-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.1%; Score 60.5; DB 4; Length 2301;
Best Local Similarity 43.6%; Pred. No. 2.9e+03;
RESULT 483
ID ABM70634 standard; protein; 3547 AA.
DE Photorhabdus luminescens protein sequence #3731.
PN W0200294867-A2.
PD 28-NOV-2002.
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PA (INSP) INST PASTEUR.
Query Match 13.1%; Score 60.5; DB 6; Length 3547;
Best Local Similarity 26.9%; Pred. No. 5.2e+03;
RESULT 484
ID ADC96773 standard; protein; 217 AA.
DE E. faecium protein sequence SEQ ID 6400.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 13.0%; Score 60; DB 7; Length 217;
Best Local Similarity 31.8%; Pred. No. 1.2e+02;
RESULT 485
ID ADJ34956 standard; protein; 225 AA.
DE Xylanase from an environmental sample seq id 172.
PN WO2003106654-A2.
PD 24-DEC-2003.
PA (DIVE-) DIVERSA CORP.
Query Match 13.0%; Score 60; DB 8; Length 225;
Best Local Similarity 29.3%; Pred. No. 1.3e+02;
RESULT 486
ID ABF59502 standard; protein; 252 AA.
DE Human interleukin-1 homologue zilla7.
PN WO200285931-A1.
PD 31-OCT-2002.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 13.0%; Score 60; DB 6; Length 252;
Best Local Similarity 28.4%; Pred. No. 1.5e+02;
RESULT 487
ID AAU91067 standard; protein; 312 AA.
DE Neisseria cell surface polypeptide #5.
PN WO200216612-A2.
PD 28-FEB-2002.
PA (MICR-) MICROSCIENCE LTD.
Query Match 13.0%; Score 60; DB 5; Length 312;
Best Local Similarity 26.3%; Pred. No. 2e+02;
RESULT 488
ID AAU91063 standard; protein; 312 AA.
DE Neisseria cell surface polypeptide #1.
PN WO200216612-A2.
PD 28-FEB-2002.
PA (MICR-) MICROSCIENCE LTD.
Query Match 13.0%; Score 60; DB 5; Length 312;
Best Local Similarity 26.3%; Pred. No. 2e+02;
RESULT 489
ID AB950022 standard; protein; 358 AA.
DE Listeria monocytogenes protein #2726.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 13.0%; Score 60; DB 5; Length 358;
Best Local Similarity 24.5%; Pred. No. 2.4e+02;
RESULT 490
ID ABU32626 standard; protein; 358 AA.
DE Protein encoded by Prokaryotic essential gene #18153.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 13.0%; Score 60; DB 6; Length 358;
Best Local Similarity 24.5%; Pred. No. 2.4e+02;
RESULT 491
ID ABG75835 standard; protein; 568 AA.
DE Transporters and ion channels protein 17, TRICH-17.
PN WO2003016493-A2.
PD 27-FEB-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 13.0%; Score 60; DB 6; Length 568;
Best Local Similarity 25.2%; Pred. No. 4.6e+02;
RESULT 492
ID ABB71755 standard; protein; 596 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 42057.
PN WO200171042-A2.
PD 27-SEP-2001.

PA (PEKE) PE CORP NY.
Query Match 13.0%; Score 60; DB 4; Length 596;
Best Local Similarity 30.0%; Pred. No. 5e+02;
RESULT 493
ID ABP62936 standard; protein; 653 AA.
DE Human polypeptide SEQ ID NO 373.
PN WO200218424-A2.
PD 07-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 13.0%; Score 60; DB 5; Length 653;
Best Local Similarity 29.6%; Pred. No. 5.6e+02;
RESULT 494
ID ABB63556 standard; protein; 1006 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 17460.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 13.0%; Score 60; DB 4; Length 1006;
Best Local Similarity 38.9%; Pred. No. 1e+03;
RESULT 495
ID AAV79167 standard; protein; 1029 AA.
DE Pneumocystis carinii major surface glycoprotein HMSG11.
PN WO200009760-A1.
PD 24-FEB-2000.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 13.0%; Score 60; DB 3; Length 1029;
Best Local Similarity 30.1%; Pred. No. 1.1e+03;
RESULT 496
ID ABU50018 standard; protein; 1039 AA.
DE Protein encoded by Prokaryotic essential gene #35545.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 13.0%; Score 60; DB 6; Length 1039;
Best Local Similarity 27.2%; Pred. No. 1.1e+03;
RESULT 497
ID AAE09365 standard; protein; 1140 AA.
DE Human ATP-binding cassette transporter ABCC6, MRP6 truncated mutant.
PN WO200162977-A2.
PD 30-AUG-2001.
PA (PXEI-) PXE INT INC.
PA (UYHA-) UNIV HAWAII.
Query Match 13.0%; Score 60; DB 4; Length 1140;
Best Local Similarity 28.4%; Pred. No. 1.2e+03;
RESULT 498
ID AAY43544 standard; protein; 1503 AA.
DE A human MFR-related ABC transporter designated MOAT-E.
PN WO9949735-A1.
PD 07-OCT-1999.
PA (FOXC-) FOX CHASE CANCER CENT.
Query Match 13.0%; Score 60; DB 2; Length 1503;
Best Local Similarity 28.4%; Pred. No. 1.8e+03;
RESULT 499
ID AAE09361 standard; protein; 1503 AA.
DE Human ATP-binding cassette transporter ABCC6 (MRP6) protein.
PN WO200162977-A2.
PD 30-AUG-2001.
PA (PXEI-) PXE INT INC.
PA (UYHA-) UNIV HAWAII.
Query Match 13.0%; Score 60; DB 4; Length 1503;
Best Local Similarity 28.4%; Pred. No. 1.8e+03;
RESULT 500
ID AAE09370 standard; protein; 1503 AA.
DE Human ATP-binding cassette transporter ABCC6 (MRP6) RI314W mutant.
PN WO200162977-A2.
PD 30-AUG-2001.
PA (PXEI-) PXE INT INC.
PA (UYHA-) UNIV HAWAII.
Query Match 13.0%; Score 60; DB 4; Length 1503;
Best Local Similarity 28.4%; Pred. No. 1.8e+03;
RESULT 501
ID AAE09367 standard; protein; 1503 AA.
DE Human ATP-binding cassette transporter ABCC6 (MRP6) VI298F mutant.
PN WO200162977-A2.

PN WO200162977-A2.
PD 30-AUG-2001.
PA (PXEI-) PXE INT INC.
PA (UYHA-) UNIV HAWAII.
Query Match 13.0%; Score 60; DB 4; Length 1503;
Best Local Similarity 28.4%; Pred. No. 1.8e+03;
RESULT 502
ID AAE09368 standard; protein; 1503 AA.
DE Human ATP-binding cassette transporter ABCC6 (MRP6) G1302R mutant.
PN WO200162977-A2.
PD 30-AUG-2001.
PA (PXEI-) PXE INT INC.
PA (UYHA-) UNIV HAWAII.
Query Match 13.0%; Score 60; DB 4; Length 1503;
Best Local Similarity 28.4%; Pred. No. 1.8e+03;
RESULT 503
ID AAE09369 standard; protein; 1503 AA.
DE Human ATP-binding cassette transporter ABCC6 (MRP6) A1303P mutant.
PN WO200162977-A2.
PD 30-AUG-2001.
PA (PXEI-) PXE INT INC.
PA (UYHA-) UNIV HAWAII.
Query Match 13.0%; Score 60; DB 4; Length 1503;
Best Local Similarity 28.4%; Pred. No. 1.8e+03;
RESULT 504
ID AAE09364 standard; protein; 1503 AA.
DE Human ATP-binding cassette transporter ABCC6 (MRP6) R1138Q mutant.
PN WO200162977-A2.
PD 30-AUG-2001.
PA (PXEI-) PXE INT INC.
PA (UYHA-) UNIV HAWAII.
Query Match 13.0%; Score 60; DB 4; Length 1503;
Best Local Similarity 28.4%; Pred. No. 1.8e+03;
RESULT 505
ID AAE09371 standard; protein; 1503 AA.
DE Human ATP-binding cassette transporter ABCC6 (MRP6) G1321I mutant.
PN WO200162977-A2.
PD 30-AUG-2001.
PA (PXEI-) PXE INT INC.
PA (UYHA-) UNIV HAWAII.
Query Match 13.0%; Score 60; DB 4; Length 1503;
Best Local Similarity 28.4%; Pred. No. 1.8e+03;
RESULT 506
ID AAE09363 standard; protein; 1503 AA.
DE Human ATP-binding cassette transporter ABCC6 (MRP6) R1114P mutant.
PN WO200162977-A2.
PD 30-AUG-2001.
PA (PXEI-) PXE INT INC.
PA (UYHA-) UNIV HAWAII.
Query Match 13.0%; Score 60; DB 4; Length 1503;
Best Local Similarity 28.4%; Pred. No. 1.8e+03;
RESULT 507
ID AAE09363 standard; protein; 1503 AA.
DE Human ATP-binding cassette transporter ABCC6 (MRP6) R1114P mutant.
PN WO200162977-A2.
PD 30-AUG-2001.
PA (PXEI-) PXE INT INC.
PA (UYHA-) UNIV HAWAII.
Query Match 13.0%; Score 60; DB 4; Length 1503;
Best Local Similarity 28.4%; Pred. No. 1.8e+03;
RESULT 508
ID ABE64864 standard; protein; 1566 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 21384.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 13.0%; Score 60; DB 4; Length 1566;
Best Local Similarity 37.1%; Pred. No. 1.9e+03;
RESULT 509
ID AAO10778 standard; protein; 141 AA.
DE Human polypeptide SEQ ID NO 24670.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.

Query Match 12.9%; Score 59.5; DB 4; Length 141;
Best Local Similarity 29.9%; Pred. No. 76;
RESULT 510
ID ABO77831 standard; protein; 237 AA.
DE Pseudomonas aeruginosa polypeptide #10006.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.9%; Score 59.5; DB 7; Length 237;
Best Local Similarity 25.5%; Pred. No. 1.6e+02;
RESULT 511
ID ADM74708 standard; protein; 248 AA.
DE Fusarium oxysporum trypsinogen-like mutant protein - Y230T.
PN WO2004029202-A2.
PD 08-APR-2004.
PA (NOVO) NOVOZYMES BIOTECH INC.
Query Match 12.9%; Score 59.5; DB 8; Length 248;
Best Local Similarity 22.0%; Pred. No. 1.7e+02;
RESULT 512
ID AAG12820 standard; protein; 257 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 12079.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 12.9%; Score 59.5; DB 3; Length 257;
Best Local Similarity 27.0%; Pred. No. 1.8e+02;
RESULT 513
ID AAG73346 standard; protein; 260 AA.
DE Human gene 1-encoded secreted protein HGBAJ60, SEQ ID NO:117.
PN WO200134628-A1.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.9%; Score 59.5; DB 4; Length 260;
Best Local Similarity 29.9%; Pred. No. 1.8e+02;
RESULT 514
ID AEG64274 standard; protein; 260 AA.
DE Human albumin fusion protein #949.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.9%; Score 59.5; DB 5; Length 260;
Best Local Similarity 29.9%; Pred. No. 1.8e+02;
RESULT 515
ID ADL77539 standard; protein; 260 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1021.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 12.9%; Score 59.5; DB 8; Length 260;
Best Local Similarity 29.9%; Pred. No. 1.8e+02;
RESULT 516
ID ADH52863 standard; protein; 275 AA.
DE Porphyromonas gulae B69 Fima protein.
PN WO2003054755-A2.
PD 03-JUL-2003.
PA (PFIZ) PFIZER PROD INC.
Query Match 12.9%; Score 59.5; DB 7; Length 275;
Best Local Similarity 27.3%; Pred. No. 1.9e+02;
RESULT 517
ID AAG40923 standard; protein; 327 AA.
DE Zea mays protein fragment SEQ ID NO: 50842.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 12.9%; Score 59.5; DB 3; Length 327;
Best Local Similarity 30.0%; Pred. No. 2.5e+02;
RESULT 518
ID AAG40922 standard; protein; 356 AA.
DE Zea mays protein fragment SEQ ID NO: 50841.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 12.9%; Score 59.5; DB 3; Length 356;
Best Local Similarity 30.0%; Pred. No. 2.8e+02;
RESULT 519

ID AAG36184 standard; protein; 361 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 44309.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 12.9%; Score 59.5; DB 3; Length 361;
Best Local Similarity 35.4%; Pred. No. 2.8e+02;
RESULT 520
ID AAG32292 standard; protein; 362 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 38929.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 12.9%; Score 59.5; DB 3; Length 362;
Best Local Similarity 35.4%; Pred. No. 2.8e+02;
RESULT 521
ID AAG36183 standard; protein; 373 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 44308.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 12.9%; Score 59.5; DB 3; Length 373;
Best Local Similarity 35.4%; Pred. No. 3e+02;
RESULT 522
ID AAG32291 standard; protein; 374 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 38928.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 12.9%; Score 59.5; DB 3; Length 374;
Best Local Similarity 35.4%; Pred. No. 3e+02;
RESULT 523
ID AAG40921 standard; protein; 450 AA.
DE Zea mays protein fragment SEQ ID NO: 50840.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 12.9%; Score 59.5; DB 3; Length 450;
Best Local Similarity 30.0%; Pred. No. 3.8e+02;
RESULT 524
ID ABB65348 standard; protein; 465 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 22836.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PERE) PE CORP NY.
Query Match 12.9%; Score 59.5; DB 4; Length 465;
Best Local Similarity 36.7%; Pred. No. 4e+02;
RESULT 525
ID ADE08499 standard; protein; 583 AA.
DE Novel protein (useful for identifying genetic disorders) #654.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 12.9%; Score 59.5; DB 7; Length 583;
Best Local Similarity 25.3%; Pred. No. 5.5e+02;
RESULT 526
ID ABU23753 standard; protein; 663 AA.
DE Protein encoded by Prokaryotic essential gene #9280.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.9%; Score 59.5; DB 6; Length 663;
Best Local Similarity 32.1%; Pred. No. 6.6e+02;
RESULT 527
ID ABU40845 standard; protein; 916 AA.
DE Protein encoded by Prokaryotic essential gene #26372.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.9%; Score 59.5; DB 6; Length 916;
Best Local Similarity 38.5%; Pred. No. 1e+03;
RESULT 528
ID ADF05449 standard; protein; 921 AA.
DE Bacterial polypeptide #1562.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.9%; Score 59.5; DB 7; Length 921;
Best Local Similarity 12.8%; Score 59; DB 4; Length 261;
Query Match 12.8%; Score 59; DB 4; Length 261;
Best Local Similarity 29.6%; Pred. No. 2.1e+02;
RESULT 529
ID AAR15159 standard; protein; 953 AA.
DE Leukotoxin from P. haemolytica.
PN US055400-A.
PD 08-OCT-1991.
PA (UYGU-) UNIV OF GUELPH.
Query Match 12.9%; Score 59.5; DB 2; Length 953;
Best Local Similarity 22.5%; Pred. No. 1.1e+03;
RESULT 530
ID ABG77195 standard; protein; 185 AA.
DE Selected Interacting Domain (SID) polypeptide #6.
PN WO200259255-A2.
PD 01-AUG-2002.
PA (HYBR-) HYBRIGENICS.
Query Match 12.8%; Score 59; DB 5; Length 185;
Best Local Similarity 38.7%; Pred. No. 1.3e+02;
RESULT 531
ID ABJ11066 standard; protein; 185 AA.
DE Yeast selected interacting domain protein SEQ ID NO: 266.
PN WO200266504-A2.
PD 29-AUG-2002.
PA (HYBR-) HYBRIGENICS.
Query Match 12.8%; Score 59; DB 5; Length 185;
Best Local Similarity 38.7%; Pred. No. 1.3e+02;
RESULT 532
ID AAB28007 standard; protein; 236 AA.
DE Human secreted protein BLAST search protein SEQ ID NO: 161.
PN WO200055171-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.8%; Score 59; DB 3; Length 236;
Best Local Similarity 36.1%; Pred. No. 1.8e+02;
RESULT 533
ID ADM74701 standard; protein; 248 AA.
DE Fusarium oxysporum trypsinogen-like mutant protein - D1985.
PN WO2004029202-A2.
PD 08-APR-2004.
PA (NOVO) NOVOZYMES BIOTECH INC.
Query Match 12.8%; Score 59; DB 8; Length 248;
Best Local Similarity 21.2%; Pred. No. 1.9e+02;
RESULT 534
ID AAM23904 standard; protein; 261 AA.
DE Human EST encoded protein SEQ ID NO: 1429.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.8%; Score 59; DB 4; Length 261;
Best Local Similarity 29.6%; Pred. No. 2.1e+02;
RESULT 535
ID AAG73381 standard; protein; 261 AA.
DE Human gene 1-encoded secreted protein HGBAJ60, SEQ ID NO:152.
PN WO200134628-A1.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.8%; Score 59; DB 4; Length 261;
Best Local Similarity 29.6%; Pred. No. 2.1e+02;
RESULT 536
ID AAB88579 standard; protein; 261 AA.
DE Human hydrophobic domain containing protein clone HP10719 #63.
PN WO200112660-A2.
PD 22-FEB-2001.
PA (SAGA) SAGAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
Query Match 12.8%; Score 59; DB 4; Length 261;
Best Local Similarity 29.6%; Pred. No. 2.1e+02;
RESULT 537
ID AAM38906 standard; protein; 261 AA.
DE Human polypeptide SEQ ID NO 2051.
PN WO20015312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.8%; Score 59; DB 4; Length 261;

Best Local Similarity 29.6%; Pred. No. 2.1e+02;
RESULT 538
ID AAB70509 standard; protein; 261 AA.
DE Angiogenesis protein endomucin protein sequence (Fig 22).
PN WO20011086-A2.
PD 15-FEB-2001.
PA (BOSB-) BOS BIOTECHNOLOGY INC.
Query Match 12.8%; Score 59; DB 4; Length 261;
Best Local Similarity 29.6%; Pred. No. 2.1e+02;
RESULT 539
ID AAB36666 standard; protein; 261 AA.
DE Human secretory protein TGC-625 SEQ ID NO:6.
PN WO200071581-A1.
PD 30-NOV-2000.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 12.8%; Score 59; DB 4; Length 261;
Best Local Similarity 29.6%; Pred. No. 2.1e+02;
RESULT 540
ID ABB89685 standard; protein; 261 AA.
DE Human polypeptide SEQ ID NO 2061.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.8%; Score 59; DB 5; Length 261;
Best Local Similarity 29.6%; Pred. No. 2.1e+02;
RESULT 541
ID ABG64273 standard; protein; 261 AA.
DE Human albumin fusion protein #948.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.8%; Score 59; DB 5; Length 261;
Best Local Similarity 29.6%; Pred. No. 2.1e+02;
RESULT 542
ID ABU03457 standard; protein; 261 AA.
DE Angiogenesis-associated human protein sequence #2.
PN WO200279492-A2.
PD 10-OCT-2002.
PA (BOSB-) BOS BIOTECHNOLOGY INC.
Query Match 12.8%; Score 59; DB 6; Length 261;
Best Local Similarity 29.6%; Pred. No. 2.1e+02;
RESULT 543
ID ADL7538 standard; protein; 261 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1020.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE//) ROSEN C A.
PA (HASE//) HASELTINE W A.
Query Match 12.8%; Score 59; DB 8; Length 261;
Best Local Similarity 29.6%; Pred. No. 2.1e+02;
RESULT 544
ID AM40692 standard; protein; 316 AA.
DE Human polypeptide SEQ ID NO 5623.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.8%; Score 59; DB 4; Length 316;
Best Local Similarity 29.6%; Pred. No. 2.7e+02;
RESULT 545
ID ABO83146 standard; protein; 415 AA.
DE Pseudomonas aeruginosa polypeptide #15321.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.8%; Score 59; DB 7; Length 415;
Best Local Similarity 30.2%; Pred. No. 4e+02;
RESULT 546
ID ABE53799 standard; protein; 499 AA.
DE Protein sequence #SEQ ID 2463.
PN EPI258494-A1.
PD 20-NOV-2002.
PA (CBLL-) CELLZOME AG.
Query Match 12.8%; Score 59; DB 6; Length 499;
Best Local Similarity 29.6%; Pred. No. 2.1e+02;
RESULT 547
ID ADK63766 standard; protein; 499 AA.
DE Disease treating protein complex-derived protein #1492.
PN EPI338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 12.8%; Score 59; DB 7; Length 499;
Best Local Similarity 32.2%; Pred. No. 5.1e+02;
RESULT 548
ID ABB70849 standard; protein; 529 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 39339.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.8%; Score 59; DB 4; Length 529;
Best Local Similarity 31.7%; Pred. No. 5.6e+02;
RESULT 549
ID ABB65057 standard; protein; 678 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 21963.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.8%; Score 59; DB 4; Length 678;
Best Local Similarity 29.5%; Pred. No. 7.9e+02;
RESULT 550
ID ABP71884 standard; protein; 694 AA.
DE Sorghum Mosaic Virus P1/HC-Pro.
PN WO2003018809-A2.
PD 06-MAR-2003.
PA (TEXA) UNIV TEXAS A & M SYSTEM.
Query Match 12.8%; Score 59; DB 6; Length 694;
Best Local Similarity 22.4%; Pred. No. 8.1e+02;
RESULT 551
ID ABB07073 standard; protein; 719 AA.
DE Bacillus thuringiensis NRS protein.
PN KR99065395-A.
PD 05-AUG-1999.
PA (KOAD) KOREA ADV INST SCI & TECHNOLOGY.
Query Match 12.8%; Score 59; DB 3; Length 719;
Best Local Similarity 27.5%; Pred. No. 8.6e+02;
RESULT 552
ID ABU27973 standard; protein; 765 AA.
DE Protein encoded by Prokaryotic essential gene #13500.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.8%; Score 59; DB 6; Length 765;
Best Local Similarity 27.7%; Pred. No. 9.3e+02;
RESULT 553
ID ADH48384 standard; protein; 936 AA.
DE Human KPP protein SEQ ID NO:42.
PN WO2004001008-A2.
PD 31-DEC-2003.
PA (INCY-) INCYTE CORP.
Query Match 12.8%; Score 59; DB 8; Length 936;
Best Local Similarity 27.3%; Pred. No. 1.2e+03;
RESULT 554
ID AAM78833 standard; protein; 970 AA.
DE Human protein SEQ ID NO 1495.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.8%; Score 59; DB 4; Length 970;
Best Local Similarity 27.3%; Pred. No. 1.3e+03;
RESULT 555
ID AAM39244 standard; protein; 970 AA.
DE Human polypeptide SEQ ID NO 2389.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.8%; Score 59; DB 4; Length 970;
Best Local Similarity 27.3%; Pred. No. 1.3e+03;

RESULT 556
ID ABP35631 standard; protein; 970 AA.
DE Fungal ZBC protein sequence #57.
PN WO200224865-A2.
PA (MICR-) MICROBIA INC.
Query Match 12.8%; Score 59; DB 5; Length 970;
Best Local Similarity 38.7%; Pred. No. 1.3e+03;
RESULT 557
ID ADJ31723 standard; protein; 970 AA.
DE Human SAK, Snk Akin Kinase.
PN US2003027756-A1.
PD 06-FEB-2003.
PA (RIGE-) RIGEL PHARM INC.
Query Match 12.8%; Score 59; DB 7; Length 970;
Best Local Similarity 27.3%; Pred. No. 1.3e+03;
RESULT 558
ID ADJ70110 standard; protein; 970 AA.
DE Human heat mitochondrial protein as a therapeutic target SegID1916.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 12.8%; Score 59; DB 7; Length 970;
Best Local Similarity 27.3%; Pred. No. 1.3e+03;
RESULT 559
ID AAM79817 standard; protein; 980 AA.
DE Human protein SEQ ID NO 3463.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.8%; Score 59; DB 4; Length 980;
Best Local Similarity 27.3%; Pred. No. 1.3e+03;
RESULT 560
ID AAM41030 standard; protein; 980 AA.
DE Human polypeptide SEQ ID NO 5961.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.8%; Score 59; DB 4; Length 980;
Best Local Similarity 27.3%; Pred. No. 1.3e+03;
RESULT 561
ID AAG82343 standard; protein; 1155 AA.
DE S. epidermidis open reading frame protein sequence SEQ ID NO:1780.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 12.8%; Score 59; DB 4; Length 1155;
Best Local Similarity 29.5%; Pred. No. 1.7e+03;
RESULT 562
ID ABU42513 standard; protein; 1633 AA.
DE Protein encoded by Prokaryotic essential gene #28040.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.8%; Score 59; DB 6; Length 1633;
Best Local Similarity 29.5%; Pred. No. 2.7e+03;
RESULT 563
ID AAY83170 standard; protein; 1802 AA.
DE Cell wall protein SdrF.
PN WO200012689-A1.
PD 09-MAR-2000.
PA (QUEE-) QUEEN ELIZABETH COLLEGE DUBLIN.
PA (TEXA) UNIV TEXAS A & M SYSTEM.
Query Match 12.8%; Score 59; DB 3; Length 1802;
Best Local Similarity 29.5%; Pred. No. 3.1e+03;
RESULT 564
ID AAY70119 standard; protein; 1802 AA.
DE Staph. epidermidis serine-aspartate repeat region protein SdrF.
PN WO200012131-A1.
PD 09-MAR-2000.
PA (INH1-) INHIBITEX INC.
PA (TEXA) UNIV TEXAS A & M SYSTEM.

PA (QUEE-) QUEEN ELIZABETH COLLEGE DUBLIN.
Query Match 12.8%; Score 59; DB 3; Length 1802;
Best Local Similarity 29.5%; Pred. No. 3.1e+03;
RESULT 565
ID ABG04711 standard; protein; 2158 AA.
DE Novel human diagnostic protein #4702.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.8%; Score 59; DB 4; Length 2158;
Best Local Similarity 26.4%; Pred. No. 4e+03;
RESULT 566
ID ABB61674 standard; protein; 2727 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 11814.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.8%; Score 59; DB 4; Length 2727;
Best Local Similarity 28.0%; Pred. No. 5.6e+03;
RESULT 567
ID AAG55957 standard; protein; 71 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 71840.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 12.7%; Score 58.5; DB 3; Length 71;
Best Local Similarity 27.5%; Pred. No. 38;
RESULT 568
ID AAG61388 standard; protein; 71 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 79619.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 12.7%; Score 58.5; DB 3; Length 71;
Best Local Similarity 27.5%; Pred. No. 38;
RESULT 569
ID AAG37425 standard; protein; 152 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 46015.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 12.7%; Score 58.5; DB 3; Length 152;
Best Local Similarity 27.3%; Pred. No. 1.1e+02;
RESULT 570
ID AAB25028 standard; peptide; 153 AA.
DE Plant SDF encoded polypeptide sequence SEQ List 2 NO:66.
PN WO200040695-A2.
PD 13-JUL-2000.
PA (CERE-) CERES INC.
Query Match 12.7%; Score 58.5; DB 3; Length 153;
Best Local Similarity 27.3%; Pred. No. 1.1e+02;
RESULT 571
ID AAY11061 standard; protein; 223 AA.
DE H. pylori ORF 09ze10333_1457137_f3_11 secreted protein.
PN WO9824475-A1.
PD 11-JUN-1998.
PA (ASTR) ASTRA AB.
Query Match 12.7%; Score 58.5; DB 2; Length 223;
Best Local Similarity 27.3%; Pred. No. 1.9e+02;
RESULT 572
ID AAU56628 standard; protein; 225 AA.
DE Propionibacterium acnes immunogenic protein #17524.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 12.7%; Score 58.5; DB 4; Length 225;
Best Local Similarity 26.1%; Pred. No. 1.9e+02;
RESULT 573
ID ABM53147 standard; protein; 225 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #17823.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 12.7%; Score 58.5; DB 6; Length 225;
Best Local Similarity 26.1%; Pred. No. 1.9e+02;
RESULT 574

ID AAV23988 standard; protein; 257 AA.
DE TON1b protein encoded by the TONNEAU1 gene.
PN WO9935269-A2.
PD 15-JUL-1999.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 12.7%; Score 58.5; DB 2; Length 257;
Best Local Similarity 20.0%; Pred. No. 2.3e+02;
RESULT 575
ID ABP23422 standard; protein; 268 AA.
DE Streptococcus polypeptide SEQ ID NO 20.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 12.7%; Score 58.5; DB 5; Length 268;
Best Local Similarity 23.5%; Pred. No. 2.5e+02;
RESULT 576
ID AAG62566 standard; protein; 344 AA.
DE Follicular conjunctivitis related adenoviral protein SEQ ID NO: 7.
PN JP2001095583-A.
PD 10-APR-2001.
PA (ITON/) ITO N.
Query Match 12.7%; Score 58.5; DB 4; Length 344;
Best Local Similarity 21.1%; Pred. No. 3.5e+02;
RESULT 577
ID AAB51257 standard; protein; 418 AA.
DE Oxalobacter formigenes OXIT protein sequence SEQ ID NO:5.
PN US6162632-A.
PD 19-DEC-2000.
PA (JOHN-) JOHNS HOPKINS SCHOOL MEDICINE.
Query Match 12.7%; Score 58.5; DB 4; Length 418;
Best Local Similarity 24.4%; Pred. No. 4.6e+02;
RESULT 578
ID ADM73109 standard; protein; 561 AA.
DE Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 1004.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPPESIGN NV.
Query Match 12.7%; Score 58.5; DB 8; Length 561;
Best Local Similarity 29.8%; Pred. No. 7e+02;
RESULT 579
ID AAE04636 standard; protein; 608 AA.
DE Pasteurella haemolytica modified leukotoxin 66 (lkt66) protein.
PN WO200144289-A2.
PD 21-JUN-2001.
PA (UYGU-) UNIV GUELPH OFFICE.
Query Match 12.7%; Score 58.5; DB 4; Length 608;
Best Local Similarity 22.5%; Pred. No. 7.8e+02;
RESULT 580
ID ADD43705 standard; protein; 786 AA.
DE Bacillus thuringiensis insecticidal protein ISP3-2245J.
PN WO2003080656-A1.
PD 02-OCT-2003.
PA (FARB) BAYER BIOSCIENCE NV.
Query Match 12.7%; Score 58.5; DB 7; Length 786;
Best Local Similarity 39.3%; Pred. No. 1.1e+03;
RESULT 581
ID AAU61465 standard; protein; 896 AA.
DE Propionibacterium acnes immunogenic protein #22361.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIAX CORP.
Query Match 12.7%; Score 58.5; DB 4; Length 896;
Best Local Similarity 28.8%; Pred. No. 1.3e+03;
RESULT 582
ID ABM57984 standard; protein; 896 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #22660.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIAX CORP.
Query Match 12.7%; Score 58.5; DB 6; Length 896;
Best Local Similarity 28.8%; Pred. No. 1.3e+03;
RESULT 583

ID AAR10889 standard; protein; 924 AA.
DE Leukotoxin 352 encoded by plasmid pAA352.
PN CA2014033-A.
PD 07-OCT-1990.
PA (UYSA-) UNIV SASKATCHEWAN.
Query Match 12.7%; Score 58.5; DB 2; Length 924;
Best Local Similarity 22.5%; Pred. No. 1.4e+03;
RESULT 584
ID AAR42378 standard; protein; 924 AA.
DE Recombinant leukotoxin peptide (split) from plasmid pGCH5.
PN WO9321323-A1.
PD 28-OCT-1993.
PA (UYSA-) UNIV SASKATCHEWAN.
Query Match 12.7%; Score 58.5; DB 2; Length 924;
Best Local Similarity 22.5%; Pred. No. 1.4e+03;
RESULT 585
ID AAR42380 standard; protein; 924 AA.
DE Recombinant leukotoxin peptide (split) from plasmid pGCH4.
PN WO9321323-A1.
PD 28-OCT-1993.
PA (UYSA-) UNIV SASKATCHEWAN.
Query Match 12.7%; Score 58.5; DB 2; Length 924;
Best Local Similarity 22.5%; Pred. No. 1.4e+03;
RESULT 586
ID AAR42385 standard; protein; 924 AA.
DE Recombinant leukotoxin peptide from plasmid pCRR28.
PN WO9321323-A1.
PD 28-OCT-1993.
PA (UYSA-) UNIV SASKATCHEWAN.
Query Match 12.7%; Score 58.5; DB 2; Length 924;
Best Local Similarity 22.5%; Pred. No. 1.4e+03;
RESULT 587
ID AAR14482 standard; protein; 926 AA.
DE LKT352.
PN WO9115237-A.
PD 17-OCT-1991.
PA (UYSA-) UNIV SASKATCHEWAN.
Query Match 12.7%; Score 58.5; DB 2; Length 926;
Best Local Similarity 22.5%; Pred. No. 1.4e+03;
RESULT 588
ID AAR34545 standard; protein; 926 AA.
DE Leukotoxin 352 produced from pAA352.
PN WO9308290-A1.
PD 29-APR-1993.
PA (UYSA-) UNIV SASKATCHEWAN.
Query Match 12.7%; Score 58.5; DB 2; Length 926;
Best Local Similarity 22.5%; Pred. No. 1.4e+03;
RESULT 589
ID AAR50291 standard; protein; 926 AA.
DE Recombinant leukotoxin from plasmid pAA352.
PN CA2093707-A.
PD 03-JAN-1994.
PA (UYSA-) UNIV SASKATCHEWAN.
Query Match 12.7%; Score 58.5; DB 2; Length 926;
Best Local Similarity 22.5%; Pred. No. 1.4e+03;
RESULT 590
ID AAW03945 standard; protein; 926 AA.
DE P. haemolytica truncated leukotoxin (LKT352).
PN WO9624675-A1.
PD 15-AUG-1996.
PA (UYSA-) UNIV SASKATCHEWAN.
Query Match 12.7%; Score 58.5; DB 2; Length 926;
Best Local Similarity 22.5%; Pred. No. 1.4e+03;
RESULT 591
ID AAW79568 standard; protein; 926 AA.
DE Leukotoxin 352 polypeptide.
PN WO9806848-A1.
PD 19-FEB-1998.
PA (UYSA-) UNIV SASKATCHEWAN.
Query Match 12.7%; Score 58.5; DB 2; Length 926;
Best Local Similarity 22.5%; Pred. No. 1.4e+03;
RESULT 592
ID AAR34547 standard; protein; 936 AA.

DE GnRH-leukotoxin gene fusion prod.
PN W09308290-A1.
PD 29-APR-1993.
PA (UYSA-) UNIV SASKATCHEWAN.
Query Match 12.7%; Score 58.5; DB 2; Length 936;
Best Local Similarity 22.5%; Pred. No. 1.4e+03;
RESULT 593
ID AAR34546 standard; protein; 943 AA.
DE Somatostatin-leukotoxin gene fusion prod.
PN W09308290-A1.
PD 29-APR-1993.
PA (UYSA-) UNIV SASKATCHEWAN.
Query Match 12.7%; Score 58.5; DB 2; Length 943;
Best Local Similarity 22.5%; Pred. No. 1.4e+03;
RESULT 594
ID AAR07167 standard; protein; 953 AA.
DE 105KD Ptx protein of P.haemolytica.
PN US4957739-A.
PD 18-SEP-1990.
PA (TEXA) UNIV OF TEXAS SYSTE.
Query Match 12.7%; Score 58.5; DB 2; Length 953;
Best Local Similarity 22.5%; Pred. No. 1.5e+03;
RESULT 595
ID AAR3865 standard; protein; 953 AA.
DE Leukotoxin protein.
PN CA2081950-A.
PD 02-MAY-1993.
PA (UYGU-) UNIV GUELPH.
Query Match 12.7%; Score 58.5; DB 2; Length 953;
Best Local Similarity 22.5%; Pred. No. 1.5e+03;
RESULT 596
ID AAR60072 standard; protein; 953 AA.
DE PtxA protein of Pasteurella haemolytica.
PN US5336491-A.
PD 09-AUG-1994.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 12.7%; Score 58.5; DB 2; Length 953;
Best Local Similarity 22.5%; Pred. No. 1.5e+03;
RESULT 597
ID AAE04638 standard; protein; 953 AA.
DE Pasteurella haemolytica leukotoxin protein.
PN W0200144289-A2.
PD 21-JUN-2001.
PA (UYGU-) UNIV GUELPH OFFICE.
Query Match 12.7%; Score 58.5; DB 4; Length 953;
Best Local Similarity 22.5%; Pred. No. 1.5e+03;
RESULT 598
ID AAW03942 standard; protein; 977 AA.
DE LKT-GnRH protein fusion from pCB113.
PN W09624675-A1.
PD 15-AUG-1996.
PA (UYSA-) UNIV SASKATCHEWAN.
Query Match 12.7%; Score 58.5; DB 2; Length 977;
Best Local Similarity 22.5%; Pred. No. 1.5e+03;
RESULT 599
ID AAW79569 standard; protein; 977 AA.
DE LKT-GnRH chimeric protein.
PN W09806948-A1.
PD 19-FEB-1998.
PA (UYSA-) UNIV SASKATCHEWAN.
Query Match 12.7%; Score 58.5; DB 2; Length 977;
Best Local Similarity 22.5%; Pred. No. 1.5e+03;
RESULT 600
ID AAR52748 standard; protein; 1069 AA.
DE Bovine IFNGamma/LKT chimeric protein encoded by plasmid pAA497.
PN US5273889-A.
PD 28-DEC-1993.
PA (UYSA-) UNIV SASKATCHEWAN.
PA (CIBA) CIBA GEIGY CANADA LTD.
Query Match 12.7%; Score 58.5; DB 2; Length 1069;
Best Local Similarity 22.5%; Pred. No. 1.7e+03;
RESULT 601
ID AAW13867 standard; protein; 1069 AA.

DE Chimeric protein #2.
PN US5594107-A.
PD 14-JAN-1997.
PA (CIBA) CIBA GEIGY CANADA LTD.
PA (UYSA-) UNIV SASKATCHEWAN.
Query Match 12.7%; Score 58.5; DB 2; Length 1069;
Best Local Similarity 22.5%; Pred. No. 1.7e+03;
RESULT 602
ID AAB21074 standard; protein; 1069 AA.
DE Bovine gamma-IFN/Pasteurella haemolytica leukotoxin fusion gene.
PN US6096320-A.
PD 01-AUG-2000.
PA (UYSA-) UNIV SASKATCHEWAN.
PA (CIBA) CIBA GEIGY CANADA LTD.
Query Match 12.7%; Score 58.5; DB 3; Length 1069;
Best Local Similarity 22.5%; Pred. No. 1.7e+03;
RESULT 603
ID AAR22103 standard; protein; 1098 AA.
DE Bovine IL-2 - LKT fusion protein.
PN W09203588-A.
PD 05-MAR-1992.
PA (POT/) POTTER A.
Query Match 12.7%; Score 58.5; DB 2; Length 1098;
Best Local Similarity 22.5%; Pred. No. 1.8e+03;
RESULT 604
ID AAR52747 standard; protein; 1098 AA.
DE Bovine IL-2/LKT chimeric protein encoded by plasmid pAA356.
PN US5273889-A.
PD 28-DEC-1993.
PA (UYSA-) UNIV SASKATCHEWAN.
PA (CIBA) CIBA GEIGY CANADA LTD.
Query Match 12.7%; Score 58.5; DB 2; Length 1098;
Best Local Similarity 22.5%; Pred. No. 1.8e+03;
RESULT 605
ID AAW13866 standard; protein; 1098 AA.
DE Chimeric protein #1.
PN US5594107-A.
PD 14-JAN-1997.
PA (CIBA) CIBA GEIGY CANADA LTD.
PA (UYSA-) UNIV SASKATCHEWAN.
Query Match 12.7%; Score 58.5; DB 2; Length 1098;
Best Local Similarity 22.5%; Pred. No. 1.8e+03;
RESULT 606
ID AAB21073 standard; protein; 1098 AA.
DE Bovine IL-2/Pasteurella haemolytica leukotoxin fusion protein.
PN US6096320-A.
PD 01-AUG-2000.
PA (UYSA-) UNIV SASKATCHEWAN.
PA (CIBA) CIBA GEIGY CANADA LTD.
Query Match 12.7%; Score 58.5; DB 3; Length 1098;
Best Local Similarity 22.5%; Pred. No. 1.8e+03;
RESULT 607
ID ABB64107 standard; protein; 1177 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 19113.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.7%; Score 58.5; DB 4; Length 1177;
Best Local Similarity 27.0%; Pred. No. 2e+03;
RESULT 608
ID ABB64105 standard; protein; 1177 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 19107.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.7%; Score 58.5; DB 4; Length 1177;
Best Local Similarity 27.0%; Pred. No. 2e+03;
RESULT 609
ID ABB66639 standard; protein; 3437 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 26709.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match
Best Local Similarity 12.7%; Score 58.5; DB 4; Length 3437;
RESULT 610
ID AA63014 standard; peptide; 20 AA.
DE Mouse lectin-1 extracellular domain antigenic peptide.
FN W09828332-A2.
PD 02-JUL-1998.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match
Best Local Similarity 12.6%; Score 58; DB 2; Length 20;
RESULT 611
ID AAU47752 standard; protein; 92 AA.
DE Propionibacterium acnes immunogenic protein #8648.
FN W0200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 12.6%; Score 58; DB 4; Length 92;
RESULT 612
ID ABM44271 standard; protein; 92 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #8947.
FN W02003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 12.6%; Score 58; DB 6; Length 92;
RESULT 613
ID ABU35562 standard; protein; 211 AA.
DE Protein encoded by Prokaryotic essential gene #21089.
FN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 12.6%; Score 58; DB 6; Length 211;
RESULT 614
ID ADH86138 standard; protein; 212 AA.
DE Enterococcus faecalis polypeptide #618.
FN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match
Best Local Similarity 12.6%; Score 58; DB 7; Length 212;
RESULT 615
ID AAR66999 standard; protein; 248 AA.
DE Trypsin-like protease.
FN W09425583-A1.
PD 10-NOV-1994.
PA (NOVO) NOVO-NORDISK AS.
Query Match
Best Local Similarity 12.6%; Score 58; DB 2; Length 248;
RESULT 616
ID AAR84716 standard; protein; 248 AA.
DE Trypsin-like Fusarium protease.
FN W09530743-A1.
PD 16-NOV-1995.
PA (NOVO) NOVO-NORDISK AS.
Query Match
Best Local Similarity 12.6%; Score 58; DB 2; Length 248;
RESULT 617
ID AAR88470 standard; protein; 248 AA.
DE Pre-pro-trypsin.
FN W09600787-A1.
PD 11-JAN-1996.
PA (NOVO) NOVO NORDISK BIOTECH INC.
Query Match
Best Local Similarity 12.6%; Score 58; DB 2; Length 249;
RESULT 618
ID AAB03659 standard; protein; 248 AA.
DE Pre-pro-trypsin amino acid sequence.
FN US6060305-A.
PD 09-MAY-2000.
PA (NOVO) NOVO NORDISK BIOTECH INC.

Query Match
Best Local Similarity 12.6%; Score 58; DB 3; Length 248;
RESULT 619
ID ADJ92130 standard; protein; 248 AA.
DE F. oxysporum trypsinogen protein.
FN US2004043455-A1.
PD 04-MAR-2004.
PA (NOVO) NOVOZYMES BIOTECH INC.
Query Match
Best Local Similarity 12.6%; Score 58; DB 8; Length 248;
RESULT 620
ID ADM74709 standard; protein; 248 AA.
DE Fusarium oxysporum trypsinogen-like mutant protein - S231P.
FN W02004029202-A2.
PD 08-APR-2004.
PA (NOVO) NOVOZYMES BIOTECH INC.
Query Match
Best Local Similarity 12.6%; Score 58; DB 8; Length 248;
RESULT 621
ID ADM74705 standard; protein; 248 AA.
DE Fusarium oxysporum trypsinogen-like mutant protein - R227S.
FN W02004029202-A2.
PD 08-APR-2004.
PA (NOVO) NOVOZYMES BIOTECH INC.
Query Match
Best Local Similarity 12.6%; Score 58; DB 8; Length 248;
RESULT 622
ID ADM74706 standard; protein; 248 AA.
DE Fusarium oxysporum trypsinogen-like mutant protein - P228T.
FN W02004029202-A2.
PD 08-APR-2004.
PA (NOVO) NOVOZYMES BIOTECH INC.
Query Match
Best Local Similarity 12.6%; Score 58; DB 8; Length 248;
RESULT 623
ID ADM74674 standard; protein; 248 AA.
DE Fusarium oxysporum trypsinogen-like wild-type protein.
FN W02004029202-A2.
PD 08-APR-2004.
PA (NOVO) NOVOZYMES BIOTECH INC.
Query Match
Best Local Similarity 12.6%; Score 58; DB 8; Length 248;
RESULT 624
ID ADM74699 standard; protein; 248 AA.
DE Fusarium oxysporum trypsinogen-like mutant protein - V144T.
FN W02004029202-A2.
PD 08-APR-2004.
PA (NOVO) NOVOZYMES BIOTECH INC.
Query Match
Best Local Similarity 12.6%; Score 58; DB 8; Length 248;
RESULT 625
ID ADM74707 standard; protein; 248 AA.
DE Fusarium oxysporum trypsinogen-like mutant protein - N229S.
FN W02004029202-A2.
PD 08-APR-2004.
PA (NOVO) NOVOZYMES BIOTECH INC.
Query Match
Best Local Similarity 12.6%; Score 58; DB 8; Length 248;
RESULT 626
ID ADM74715 standard; protein; 249 AA.
DE Fusarium oxysporum trypsinogen-like mutant protein - G224GT.
FN W02004029202-A2.
PD 08-APR-2004.
PA (NOVO) NOVOZYMES BIOTECH INC.
Query Match
Best Local Similarity 12.6%; Score 58; DB 8; Length 249;
RESULT 627
ID ABUL5870 standard; protein; 260 AA.
DE Protein encoded by Prokaryotic essential gene #1397.
FN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 12.6%; Score 58; DB 6; Length 260;

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Best Local Similarity 25.2%; Pred. No. 2.7e+02;
RESULT 628
ID ABP25421 standard; protein; 267 AA.
DE Streptococcus polypeptide SEQ ID NO 18.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 12.6%; Score 58; DB 5; Length 267;
Best Local Similarity 24.4%; Pred. No. 2.8e+02;
RESULT 629
ID ABO82792 standard; protein; 279 AA.
DE Pseudomonas aeruginosa polypeptide #14967.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.6%; Score 58; DB 7; Length 279;
Best Local Similarity 32.3%; Pred. No. 3e+02;
RESULT 630
ID ADG15013 standard; protein; 334 AA.
DE Human SECP-46 protein.
PN WO2003087300-A2.
PD 23-OCT-2003.
PA (INCY-) INCYTE CORP.
Query Match 12.6%; Score 58; DB 7; Length 334;
Best Local Similarity 28.6%; Pred. No. 3.9e+02;
RESULT 631
ID AAE06605 standard; protein; 350 AA.
DE Human protein having hydrophobic domain, HP10793.
PN WO200149728-A2.
PD 12-JUL-2001.
PA (PROT-) PROTEGENE INC.
PA (SAGA ) SAGAMI CHEM RES CENT.
Query Match 12.6%; Score 58; DB 4; Length 350;
Best Local Similarity 28.6%; Pred. No. 4.1e+02;
RESULT 632
ID AAB92578 standard; protein; 351 AA.
DE Human protein sequence SEQ ID NO:10798.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 12.6%; Score 58; DB 4; Length 351;
Best Local Similarity 28.6%; Pred. No. 4.2e+02;
RESULT 633
ID AAY73431 standard; protein; 366 AA.
DE Human secreted protein clone yb186_1 protein sequence SEQ ID NO:84.
PN WO9958642-A2.
PD 18-NOV-1999.
PA (GEMY ) GENETICS INST INC.
Query Match 12.6%; Score 58; DB 3; Length 366;
Best Local Similarity 28.6%; Pred. No. 4.4e+02;
RESULT 634
ID ABU20572 standard; protein; 405 AA.
DE Protein encoded by Prokaryotic essential gene #6099.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.6%; Score 58; DB 6; Length 405;
Best Local Similarity 33.3%; Pred. No. 5.1e+02;
RESULT 635
ID AAW34319 standard; protein; 415 AA.
DE Beta-2 adrenalin receptor subtype.
PN WO9735963-A1.
PD 02-OCT-1997.
PA (DAIN ) DAINIPPON PHARM CO LTD.
Query Match 12.6%; Score 58; DB 2; Length 415;
Best Local Similarity 34.8%; Pred. No. 5.3e+02;
RESULT 636
ID ABU43394 standard; protein; 423 AA.
DE Protein encoded by Prokaryotic essential gene #28921.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.6%; Score 58; DB 2; Length 596;
Best Local Similarity 27.1%; Pred. No. 5.4e+02;
RESULT 637
ID ABU39967 standard; protein; 425 AA.
DE Protein encoded by Prokaryotic essential gene #25494.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.6%; Score 58; DB 6; Length 425;
Best Local Similarity 32.2%; Pred. No. 5.4e+02;
RESULT 638
ID ABB53578 standard; protein; 439 AA.
DE Lactococcus lactis protein acma.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.
Query Match 12.6%; Score 58; DB 5; Length 439;
Best Local Similarity 31.9%; Pred. No. 5.7e+02;
RESULT 639
ID ABB05727 standard; protein; 455 AA.
DE Human signal transduction protein clone tes3_5k22.
PN WO200198454-A2.
PD 27-DEC-2001.
PA (GERH-) GERMAN HUMAN GENOME PROJECT.
Query Match 12.6%; Score 58; DB 5; Length 455;
Best Local Similarity 25.5%; Pred. No. 6e+02;
RESULT 640
ID AAB12529 standard; protein; 463 AA.
DE Human Mas protein SEQ ID NO:13.
PN JP2000146982-A.
PD 26-MAY-2000.
PA (SLOK ) SLOAN KETTERING INST CANCER RES.
Query Match 12.6%; Score 58; DB 3; Length 463;
Best Local Similarity 25.5%; Pred. No. 6.1e+02;
RESULT 641
ID AAB42315 standard; protein; 463 AA.
DE Human ORFX ORF2079 polypeptide sequence SEQ ID NO:4158.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 12.6%; Score 58; DB 3; Length 463;
Best Local Similarity 25.5%; Pred. No. 6.1e+02;
RESULT 642
ID ABG01678 standard; protein; 470 AA.
DE Novel human diagnostic protein #1669.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.6%; Score 58; DB 4; Length 470;
Best Local Similarity 27.3%; Pred. No. 6.3e+02;
RESULT 643
ID AAW48788 standard; protein; 564 AA.
DE Thyroid peroxidase deletion mutant 7.
PN WO9820354-A2.
PD 14-MAY-1998.
PA (RSRR-) RSR LTD.
Query Match 12.6%; Score 58; DB 2; Length 564;
Best Local Similarity 26.9%; Pred. No. 8.1e+02;
RESULT 644
ID ABG00360 standard; protein; 571 AA.
DE Novel human diagnostic protein #351.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.6%; Score 58; DB 4; Length 571;
Best Local Similarity 28.2%; Pred. No. 8.2e+02;
RESULT 645
ID AAW48785 standard; protein; 596 AA.
DE Thyroid peroxidase deletion mutant 4.
PN WO9820354-A2.
PD 14-MAY-1998.
PA (RSRR-) RSR LTD.
Query Match 12.6%; Score 58; DB 2; Length 596;
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Best Local Similarity 26.9%; Pred. No. 8.7e+02;
RESULT 646
ID AAB64031 standard; protein; 599 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 18885.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PKKE) PE CORP NY.
Query Match 12.6%; Score 58; DB 4; Length 599;
Best Local Similarity 38.6%; Pred. No. 8.8e+02;
RESULT 647
ID AAW48789 standard; protein; 624 AA.
DE Thyroid peroxidase deletion mutant 8.
PN WO9820354-A2.
PD 14-MAY-1998.
PA (RSRR-) RSR LTD.
Query Match 12.6%; Score 58; DB 2; Length 624;
Best Local Similarity 26.9%; Pred. No. 9.3e+02;
RESULT 648
ID ADA34734 standard; protein; 659 AA.
DE Acinetobacter baumannii protein #1895.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.6%; Score 58; DB 6; Length 659;
Best Local Similarity 32.6%; Pred. No. 1e+03;
RESULT 649
ID AAW48786 standard; protein; 681 AA.
DE Thyroid peroxidase deletion mutant 5.
PN WO9820354-A2.
PD 14-MAY-1998.
PA (RSRR-) RSR LTD.
Query Match 12.6%; Score 58; DB 2; Length 681;
Best Local Similarity 26.9%; Pred. No. 1.1e+03;
RESULT 650
ID AAW48787 standard; protein; 689 AA.
DE Thyroid peroxidase deletion mutant 7.
PN WO9820354-A2.
PD 14-MAY-1998.
PA (RSRR-) RSR LTD.
Query Match 12.6%; Score 58; DB 2; Length 689;
Best Local Similarity 26.9%; Pred. No. 1.1e+03;
RESULT 651
ID AAW48790 standard; protein; 740 AA.
DE Thyroid peroxidase deletion mutant 9.
PN WO9820354-A2.
PD 14-MAY-1998.
PA (RSRR-) RSR LTD.
Query Match 12.6%; Score 58; DB 2; Length 740;
Best Local Similarity 26.9%; Pred. No. 1.2e+03;
RESULT 652
ID AAW35390 standard; protein; 774 AA.
DE Flavobacterium odoratum isoamylase.
PN JP08023981-A.
PD 30-JAN-1996.
PA (NISO) NIPPON SHOKUIN KAKO KK.
Query Match 12.6%; Score 58; DB 2; Length 774;
Best Local Similarity 34.0%; Pred. No. 1.3e+03;
RESULT 653
ID ADP30359 standard; protein; 829 AA.
DE Human secreted protein SEQ ID #1126.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 12.6%; Score 58; DB 8; Length 829;
Best Local Similarity 30.4%; Pred. No. 1.4e+03;
RESULT 654
ID AAY07733 standard; protein; 848 AA.
DE Human thyroid peroxidase htpo protein.
PN JP11094833-A.
PD 09-APR-1999.
PA (SRLS-) SRL KK.
Query Match 12.6%; Score 58; DB 2; Length 848;
Best Local Similarity 26.9%; Pred. No. 1.4e+03;
RESULT 655
ID AAW48782 standard; protein; 852 AA.
DE Thyroid peroxidase deletion mutant.
PN WO9820354-A2.
PD 14-MAY-1998.
PA (RSRR-) RSR LTD.
Query Match 12.6%; Score 58; DB 2; Length 852;
Best Local Similarity 26.9%; Pred. No. 1.4e+03;
RESULT 656
ID AAW48791 standard; protein; 881 AA.
DE Thyroid peroxidase deletion mutant 10.
PN WO9820354-A2.
PD 14-MAY-1998.
PA (RSRR-) RSR LTD.
Query Match 12.6%; Score 58; DB 2; Length 881;
Best Local Similarity 26.9%; Pred. No. 1.5e+03;
RESULT 657
ID ADE47732 standard; protein; 888 AA.
DE Human NOV30a protein SEQ ID NO:94.
PN WO2003076642-A2.
PD 18-SEP-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.6%; Score 58; DB 7; Length 888;
Best Local Similarity 26.9%; Pred. No. 1.5e+03;
RESULT 658
ID ADJ79002 standard; protein; 888 AA.
DE Human NOVX protein Nov30A amino acid sequence.
PN US2004014053-A1.
PD 22-JAN-2004.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (KEKU/) KEKUDA R.
PA (MILL/) MILLER C E.
PA (RIEG/) RIEGER D K.
PA (PENA/) PENA C E A.
PA (SHIM/) SHIMKETS R A.
PA (LILL/) LI L.
PA (BERG/) BERGHS C.
PA (ZHON/) ZHONG M.
PA (CASW/) CASMAN S J.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDOG F L.
PA (PADI/) PADIGARU M.
PA (SMIT/) SMITHSON G.
PA (JTWI/) JI W.
PA (GORM/) GORMAN L.
PA (VERN/) VERNET C A M.
PA (LEIT/) LEITE M W.
PA (GUOX/) GUO X S.
PA (ANDE/) ANDERSON D W.
PA (SPYT/) SPYTEK K A.
PA (GERL/) GERLACH V.
PA (BURG/) BURGESS C E.
PA (KHRA/) KHRAMTSOV N V.
PA (ORTT/) ORT T.
PA (ELLE/) ELLERMAN K.
PA (RAST/) RASTELLI L.
PA (AGEE/) AGEE M L.
PA (CHAU/) CHAUDHURI A.
PA (CHAN/) CHANT J S.
PA (DIPI/) DIPIPO V A.
PA (EDIN/) EDINGER S R.
PA (EISE/) EISEN A J.
PA (GANG/) GANGOLLI E A.
PA (GIOT/) GIOT L.
PA (OOIC/) OOI C E.
PA (ROTH/) ROTHENBERG M E.
PA (SPAD/) SPADERNA S K.
PA (HUAL/) HUALT T.
PA (LIUX/) LIU X.
PA (TAUP/) TAUPIER R J.
PA (CATT/) CATTERTON E.
PA (SHEN/) SHENOY S G.

Query Match 12.6%; Score 58; DB 8; Length 888;
Best Local Similarity 26.9%; Pred. No. 1.5e+03;
RESULT 659
ID ABU70701 standard; protein; 903 AA.
DE Human adipocyte Selected Interacting domain, SID, #332.
PN WO200286122-A2.
PD 31-OCT-2002.
PA (HYBR-) HYBRIGENICS.
Query Match 12.6%; Score 58; DB 6; Length 903;
Best Local Similarity 30.4%; Pred. No. 1.6e+03;
RESULT 660
ID AAR44615 standard; protein; 933 AA.
DE Human thyroid peroxidase.
PN WO9323073-A1.
PD 25-NOV-1993.
PA (UNMI) UNIV MICHIGAN.
Query Match 12.6%; Score 58; DB 2; Length 933;
Best Local Similarity 26.9%; Pred. No. 1.6e+03;
RESULT 661
ID AAR75689 standard; protein; 933 AA.
DE Human thyroid peroxidase.
PN EP65502-A1.
PD 31-MAY-1995.
PA (NIUS) NIPPON SUISAN KAISHA LTD.
PA (NISR) NISSUI PHARM CO LTD.
Query Match 12.6%; Score 58; DB 2; Length 933;
Best Local Similarity 26.9%; Pred. No. 1.6e+03;
RESULT 662
ID AAW48781 standard; protein; 948 AA.
DE Thyroid peroxidase.
PN WO9820354-A2.
PD 14-MAY-1998.
PA (RSRR-) RSR LTD.
Query Match 12.6%; Score 58; DB 2; Length 948;
Best Local Similarity 26.9%; Pred. No. 1.7e+03;
RESULT 663
ID ADP30360 standard; protein; 993 AA.
DE Human secreted protein SEQ ID #127.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 12.6%; Score 58; DB 8; Length 993;
Best Local Similarity 30.4%; Pred. No. 1.8e+03;
RESULT 664
ID AAG91409 standard; protein; 1221 AA.
DE C. glutamicum protein fragment SEQ ID NO: 5163.
PN EP1108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 12.6%; Score 58; DB 4; Length 1221;
Best Local Similarity 38.8%; Pred. No. 2.4e+03;
RESULT 665
ID AEG80321 standard; protein; 1221 AA.
DE C. glutamicum metabolic pathway (MP) protein #1.
PN WO200251231-A1.
PD 04-JUL-2002.
PA (BADI) BASF AG.
Query Match 12.6%; Score 58; DB 5; Length 1221;
Best Local Similarity 38.8%; Pred. No. 2.4e+03;
RESULT 666
ID AAEL8908 standard; protein; 1221 AA.
DE Corynebacterium glutamicum homocysteine methyltransferase II (meth).
PN WO200210209-A1.
PD 07-FEB-2002.
PA (DEGS) DEGUSSA AG.
Query Match 12.6%; Score 58; DB 5; Length 1221;
Best Local Similarity 38.8%; Pred. No. 2.4e+03;
RESULT 667
ID ADD13589 standard; protein; 1221 AA.
DE C. glutamicum metabolic pathway protein RXA04186.
PN WO2003040681-A2.
PD 15-MAY-2003.
PA (BADI) BASF AG.

Query Match 12.6%; Score 58; DB 7; Length 1221;
Best Local Similarity 38.8%; Pred. No. 2.4e+03;
RESULT 668
ID ADD25207 standard; protein; 1323 AA.
DE Fertility restorer protein #41.
PN WO2003006622-A2.
PD 23-JAN-2003.
PA (UYMC-) UNIV MCGILL.
PA (DNAL-) DNA LANDMARKS INC.
Query Match 12.6%; Score 58; DB 7; Length 1323;
Best Local Similarity 31.4%; Pred. No. 2.7e+03;
RESULT 669
ID ADN61222 standard; protein; 1323 AA.
DE Radish nuclear fertility restorer Rfo protein SEQ ID NO:81.
PN WO2004006655-A2.
PD 22-JAN-2004.
PA (UYMC-) UNIV MCGILL.
PA (DNAL-) DNA LANDMARKS INC.
PA (BADI) BASF PLANT SCI GMBH.
Query Match 12.6%; Score 58; DB 8; Length 1323;
Best Local Similarity 31.4%; Pred. No. 2.7e+03;
RESULT 670
ID ABM67717 standard; protein; 2951 AA.
DE Photorhabdus luminescens protein sequence #814.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 12.6%; Score 58; DB 6; Length 2951;
Best Local Similarity 32.4%; Pred. No. 8.2e+03;
RESULT 671
ID ABM70325 standard; protein; 3041 AA.
DE Photorhabdus luminescens protein sequence #3422.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 12.6%; Score 58; DB 6; Length 3041;
Best Local Similarity 32.4%; Pred. No. 8.6e+03;
RESULT 672
ID ADM68813 standard; protein; 4868 AA.
DE Mosquito ryanodine receptor related protein SEQ ID NO:57.
PN WO2004027042-A2.
PD 01-APR-2004.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 12.6%; Score 58; DB 8; Length 4868;
Best Local Similarity 29.9%; Pred. No. 1.7e+04;
RESULT 673
ID AAW70380 standard; protein; 137 AA.
DE Anti-human CD23 5E8 monoclonal antibody heavy chain variable region.
PN WO9837099-A1.
PD 27-AUG-1998.
PA (IDEC) IDEC PHARM CORP.
PA (SEKG) SEIKAGAKU CORP.
Query Match 12.4%; Score 57.5; DB 2; Length 137;
Best Local Similarity 21.1%; Pred. No. 1.3e+02;
RESULT 674
ID ADK35270 standard; protein; 139 AA.
DE Novel human polypeptide SeqID7352.
PN WO200216439-A2.
PD 28-FEB-2002.
PA (HYSE-) HYSEQ INC.
Query Match 12.4%; Score 57.5; DB 5; Length 139;
Best Local Similarity 32.0%; Pred. No. 1.3e+02;
RESULT 675
ID AAG00150 standard; protein; 150 AA.
DE Human secreted protein, SEQ ID NO: 4231.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 12.4%; Score 57.5; DB 3; Length 150;
Best Local Similarity 28.0%; Pred. No. 1.5e+02;
RESULT 676

ID AAW38521 standard; protein; 181 AA.
DE S. pneumoniae glutamine transport ATP-binding protein.
PN W09743303-A1.
PD 20-NOV-1997.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 12.4%; Score 57.5; DB 2; Length 181;
Best Local Similarity 30.1%; Pred. No. 1.9e+02;
RESULT 677
ID ABU0809 standard; protein; 246 AA.
DE S. pneumoniae type 4 strain protein from coding region #377.
PN W0200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 12.4%; Score 57.5; DB 6; Length 246;
Best Local Similarity 30.1%; Pred. No. 2.9e+02;
RESULT 678
ID ADK48198 standard; protein; 246 AA.
DE Streptococcus pneumoniae protein, Seq ID NO 4713.
PN US6699703-B1.
PD 02-MAR-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.4%; Score 57.5; DB 8; Length 246;
Best Local Similarity 30.1%; Pred. No. 2.9e+02;
RESULT 679
ID AAY81630 standard; protein; 247 AA.
DE Streptococcus pneumoniae type 4 protein sequence #130.
PN W0200006737-A2.
PD 10-FEB-2000.
PA (MTCR-) MICROBIAL TECHNIQS LTD.
Query Match 12.4%; Score 57.5; DB 3; Length 247;
Best Local Similarity 30.1%; Pred. No. 2.9e+02;
RESULT 680
ID AAG14193 standard; protein; 307 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 13961.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 12.4%; Score 57.5; DB 3; Length 307;
Best Local Similarity 32.3%; Pred. No. 4e+02;
RESULT 681
ID AAG14192 standard; protein; 315 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 13960.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 12.4%; Score 57.5; DB 3; Length 315;
Best Local Similarity 32.3%; Pred. No. 4.1e+02;
RESULT 682
ID AAG10918 standard; protein; 329 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 9435.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 12.4%; Score 57.5; DB 3; Length 329;
Best Local Similarity 37.2%; Pred. No. 4.4e+02;
RESULT 683
ID AAG36733 standard; protein; 329 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 45058.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 12.4%; Score 57.5; DB 3; Length 329;
Best Local Similarity 37.2%; Pred. No. 4.4e+02;
RESULT 684
ID ABB91746 standard; protein; 329 AA.
DE Herbigidally active polypeptide SEQ ID NO 957.
PN W0200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 12.4%; Score 57.5; DB 5; Length 329;
Best Local Similarity 37.2%; Pred. No. 4.4e+02;
RESULT 685
ID ADB65204 standard; protein; 344 AA.
DE Human protein encoded by clone SPLN20201830.
PN EPI308459-A2.
PD 12-JUN-2003.
PA (KASE/) KASER M R.
Query Match 12.4%; Score 57.5; DB 4; Length 475;
Best Local Similarity 30.3%; Pred. No. 7.3e+02;
RESULT 686
ID AAG36732 standard; protein; 380 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 45057.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 12.4%; Score 57.5; DB 3; Length 380;
Best Local Similarity 37.2%; Pred. No. 5.3e+02;
RESULT 687
ID AAG10917 standard; protein; 380 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 9434.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 12.4%; Score 57.5; DB 3; Length 380;
Best Local Similarity 37.2%; Pred. No. 5.3e+02;
RESULT 688
ID AAG14191 standard; protein; 413 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 13959.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 12.4%; Score 57.5; DB 3; Length 413;
Best Local Similarity 32.3%; Pred. No. 6e+02;
RESULT 689
ID ABB91616 standard; protein; 413 AA.
DE Herbigidally active polypeptide SEQ ID NO 827.
PN W0200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 12.4%; Score 57.5; DB 5; Length 413;
Best Local Similarity 32.3%; Pred. No. 6e+02;
RESULT 690
ID ABP29219 standard; protein; 446 AA.
DE Streptococcus polypeptide SEQ ID NO 7614.
PN W0200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 12.4%; Score 57.5; DB 5; Length 446;
Best Local Similarity 37.3%; Pred. No. 6.7e+02;
RESULT 691
ID ABUL6196 standard; protein; 452 AA.
DE Protein encoded by Prokaryotic essential gene #1723.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.4%; Score 57.5; DB 6; Length 452;
Best Local Similarity 25.3%; Pred. No. 6.8e+02;
RESULT 692
ID AAM78493 standard; protein; 453 AA.
DE Human protein SEQ ID NO 1155.
PN W0200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.4%; Score 57.5; DB 4; Length 453;
Best Local Similarity 28.0%; Pred. No. 6.8e+02;
RESULT 693
ID ABB71851 standard; protein; 475 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 42345.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.4%; Score 57.5; DB 4; Length 475;
Best Local Similarity 30.3%; Pred. No. 7.3e+02;
RESULT 694
ID ADE76868 standard; protein; 488 AA.
DE Human protein expressed in a liver disorder #11.
PN US2003108871-A1.
PD 12-JUN-2003.
PA (KASE/) KASER M R.

Query Match 12.4%; Score 57.5; DB 8; Length 488;
Best Local Similarity 28.0%; Pred. No. 7.6e+02;
RESULT 695
ID AAR2243 standard; protein; 491 AA.
DE Human fibrinogen B-beta chain protein.
PN WO9523868-A1.
PD 08-SEP-1995.
PA (ZYMO) ZYMOGENETICS INC.
PA (PHAR-) PHARM PROTEINS LTD.
Query Match 12.4%; Score 57.5; DB 2; Length 491;
Best Local Similarity 28.0%; Pred. No. 7.7e+02;
RESULT 696
ID AAM78492 standard; protein; 491 AA.
DE Human protein SEQ ID NO 1154.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.4%; Score 57.5; DB 4; Length 491;
Best Local Similarity 28.0%; Pred. No. 7.7e+02;
RESULT 697
ID AAE36413 standard; protein; 491 AA.
DE Human FBG reference protein (GI 11761631).
PN WO2003020118-A2.
PD 13-MAR-2003.
PA (VITI-) VITIVITY INC.
Query Match 12.4%; Score 57.5; DB 6; Length 491;
Best Local Similarity 28.0%; Pred. No. 7.7e+02;
RESULT 698
ID ADP65229 standard; protein; 491 AA.
DE Human fibrinogen, beta chain preproprotein, fibrinogen, B beta protein.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 12.4%; Score 57.5; DB 7; Length 491;
Best Local Similarity 28.0%; Pred. No. 7.7e+02;
RESULT 699
ID ADP65300 standard; protein; 491 AA.
DE Human fibrinogen, beta chain preproprotein.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 12.4%; Score 57.5; DB 7; Length 491;
Best Local Similarity 28.0%; Pred. No. 7.7e+02;
RESULT 700
ID AAM79475 standard; protein; 495 AA.
DE Human protein SEQ ID NO 3121.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.4%; Score 57.5; DB 4; Length 495;
Best Local Similarity 28.0%; Pred. No. 7.7e+02;
RESULT 701
ID AAM79476 standard; protein; 495 AA.
DE Human protein SEQ ID NO 3122.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.4%; Score 57.5; DB 4; Length 495;
Best Local Similarity 28.0%; Pred. No. 7.7e+02;
RESULT 702
ID AAM79477 standard; protein; 495 AA.
DE Human protein SEQ ID NO 3123.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.4%; Score 57.5; DB 4; Length 495;
Best Local Similarity 28.0%; Pred. No. 7.7e+02;
RESULT 703
ID ABB62075 standard; protein; 509 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 13017.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PERE) PE CORP NY.

Query Match 12.4%; Score 57.5; DB 4; Length 509;
Best Local Similarity 30.5%; Pred. No. 8.1e+02;
RESULT 704
ID ABP6247 standard; protein; 515 AA.
DE Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:991.
PN EP1227152-A1.
PD 31-JUL-2002.
PA (NEST) SOC PROD NESTLE SA.
Query Match 12.4%; Score 57.5; DB 5; Length 515;
Best Local Similarity 27.5%; Pred. No. 8.2e+02;
RESULT 705
ID ABU43576 standard; protein; 786 AA.
DE Protein encoded by Prokaryotic essential gene #29103.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.4%; Score 57.5; DB 6; Length 786;
Best Local Similarity 25.0%; Pred. No. 1.5e+03;
RESULT 706
ID ADD43703 standard; protein; 788 AA.
DE Bacillus thuringiensis insecticidal protein ISP3-327D.
PN WO2003080656-A1.
PD 02-OCT-2003.
PA (FARB) BAYER BIOSCIENCE NV.
Query Match 12.4%; Score 57.5; DB 7; Length 788;
Best Local Similarity 39.2%; Pred. No. 1.5e+03;
RESULT 707
ID ADN08753 standard; protein; 788 AA.
DE B. thuringiensis Vip3c SEQ ID NO:2.
PN WO2003075655-A2.
PD 18-SEP-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 12.4%; Score 57.5; DB 7; Length 788;
Best Local Similarity 39.2%; Pred. No. 1.5e+03;
RESULT 708
ID ADN08783 standard; protein; 788 AA.
DE B. thuringiensis vip3c-12168 protein SEQ ID NO:32.
PN WO2003075655-A2.
PD 18-SEP-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 12.4%; Score 57.5; DB 7; Length 788;
Best Local Similarity 39.2%; Pred. No. 1.5e+03;
RESULT 709
ID AAM46862 standard; protein; 789 AA.
DE Bacillus thuringiensis toxin designated 86BBI(c).
PN WO9800546-A2.
PD 08-JAN-1998.
PA (MYCO) MYCOGEN CORP.
Query Match 12.4%; Score 57.5; DB 2; Length 789;
Best Local Similarity 39.2%; Pred. No. 1.5e+03;
RESULT 710
ID AAM46870 standard; protein; 789 AA.
DE Bacillus thuringiensis toxin designated 29HD(a).
PN WO9800546-A2.
PD 08-JAN-1998.
PA (MYCO) MYCOGEN CORP.
Query Match 12.4%; Score 57.5; DB 2; Length 789;
Best Local Similarity 39.2%; Pred. No. 1.5e+03;
RESULT 711
ID AAM46863 standard; protein; 789 AA.
DE Bacillus thuringiensis toxin designated 86V1(a).
PN WO9800546-A2.
PD 08-JAN-1998.
PA (MYCO) MYCOGEN CORP.
Query Match 12.4%; Score 57.5; DB 2; Length 789;
Best Local Similarity 39.2%; Pred. No. 1.5e+03;
RESULT 712
ID AAM46867 standard; protein; 789 AA.
DE Bacillus thuringiensis toxin designated 202S(a).
PN WO9800546-A2.
PD 08-JAN-1998.
PA (MYCO) MYCOGEN CORP.
Query Match 12.4%; Score 57.5; DB 2; Length 789;
Best Local Similarity 39.2%; Pred. No. 1.5e+03;
RESULT 713
ID AAM46867 standard; protein; 789 AA.
DE Bacillus thuringiensis toxin designated 202S(a).
PN WO9800546-A2.
PD 08-JAN-1998.
PA (MYCO) MYCOGEN CORP.
Query Match 12.4%; Score 57.5; DB 2; Length 789;

Best Local Similarity 39.2%; Pred. No. 1.5e+03;
RESULT 713
ID AAY24966 standard; protein; 789 AA.
DE Bacillus thuringiensis toxin 86VI(a).
PN WO9933991-A2.
PD 08-JUL-1999.
PA (MYCO) MYCOGEN CORP.
Query Match 12.4%; Score 57.5; DB 2; Length 789;
Best Local Similarity 39.2%; Pred. No. 1.5e+03;
RESULT 714
ID AAY24970 standard; protein; 789 AA.
DE Bacillus thuringiensis toxin 202S(a).
PN WO9933991-A2.
PD 08-JUL-1999.
PA (MYCO) MYCOGEN CORP.
Query Match 12.4%; Score 57.5; DB 2; Length 789;
Best Local Similarity 39.2%; Pred. No. 1.5e+03;
RESULT 715
ID AAY24965 standard; protein; 789 AA.
DE Bacillus thuringiensis toxin 86BBI(c).
PN WO9933991-A2.
PD 08-JUL-1999.
PA (MYCO) MYCOGEN CORP.
Query Match 12.4%; Score 57.5; DB 2; Length 789;
Best Local Similarity 39.2%; Pred. No. 1.5e+03;
RESULT 716
ID AAY24973 standard; protein; 789 AA.
DE Bacillus thuringiensis toxin 29HD(a).
PN WO9933991-A2.
PD 08-JUL-1999.
PA (MYCO) MYCOGEN CORP.
Query Match 12.4%; Score 57.5; DB 2; Length 789;
Best Local Similarity 39.2%; Pred. No. 1.5e+03;
RESULT 717
ID AAY46872 standard; protein; 790 AA.
DE Bacillus thuringiensis toxin designated 129HG(b).
PN WO9800546-A2.
PD 08-JAN-1998.
PA (MYCO) MYCOGEN CORP.
Query Match 12.4%; Score 57.5; DB 2; Length 790;
Best Local Similarity 39.2%; Pred. No. 1.5e+03;
RESULT 718
ID AAY24975 standard; protein; 790 AA.
DE Bacillus thuringiensis toxin 129HD(b).
PN WO9933991-A2.
PD 08-JUL-1999.
PA (MYCO) MYCOGEN CORP.
Query Match 12.4%; Score 57.5; DB 2; Length 790;
Best Local Similarity 39.2%; Pred. No. 1.5e+03;
RESULT 719
ID ABG09102 standard; protein; 841 AA.
DE Novel human diagnostic protein #9093.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.4%; Score 57.5; DB 4; Length 841;
Best Local Similarity 24.3%; Pred. No. 1.6e+03;
RESULT 720
ID AAR34548 standard; protein; 951 AA.
DE Rotavirus VP4-leukotoxin gene fusion prod.
PN WO9308290-A1.
PD 29-APR-1993.
PA (UYSA-) UNIV SASKATCHEWAN.
Query Match 12.4%; Score 57.5; DB 2; Length 951;
Best Local Similarity 22.5%; Pred. No. 1.9e+03;
RESULT 721
ID ABW69148 standard; protein; 984 AA.
DE Photorhabdus luminescens protein sequence #2245.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 12.4%; Score 57.5; DB 6; Length 984;

Best Local Similarity 33.3%; Pred. No. 2e+03;
RESULT 722
ID AAF59923 standard; protein; 2938 AA.
DE GAP protein Iral.
PN WO9416069-A2.
PD 21-JUL-1994.
PA (SCHE) SCHERING CORP.
Query Match 12.4%; Score 57.5; DB 2; Length 2938;
Best Local Similarity 24.3%; Pred. No. 9.4e+03;
RESULT 723
ID ADP88187 standard; protein; 4760 AA.
DE Aspergillus oryzae peptide synthetase protein.
PN JP2004180534-A.
PD 02-JUL-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN SANGYO GIJUTSU SO.
PA (DOKU-) DOKURITSU GYOSEI HOJIN SEIHIN HYOKA GIJU.
PA (DOKU-) DOKURITSU GYOSEI HOJIN SHURUI SOGO KENKY.
PA (GEKK-) GEKKEIKAN KK.
Query Match 12.4%; Score 57.5; DB 8; Length 4760;
Best Local Similarity 22.2%; Pred. No. 1.8e+04;
RESULT 724
ID ADG90810 standard; protein; 138 AA.
DE Hepatic specific nucleic acid protein #201.
PN WO2003066877-A2.
PD 14-AUG-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 12.3%; Score 57; DB 7; Length 138;
Best Local Similarity 36.0%; Pred. No. 1.5e+02;
RESULT 725
ID ABU02067 standard; protein; 158 AA.
DE S. pneumoniae type 4 strain protein from coding region #1644.
PN WO200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 12.3%; Score 57; DB 6; Length 158;
Best Local Similarity 21.9%; Pred. No. 1.8e+02;
RESULT 726
ID ADK46757 standard; protein; 158 AA.
DE Streptococcus pneumoniae protein, Seq ID No 3272.
PN US6699703-B1.
PD 02-MAR-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.3%; Score 57; DB 8; Length 158;
Best Local Similarity 21.9%; Pred. No. 1.8e+02;
RESULT 727
ID AAE05353 standard; protein; 247 AA.
DE Mouse high affinity immunoglobulin epsilon receptor beta-subunit protein.
PN WO200148192-A1.
PD 05-JUL-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 12.3%; Score 57; DB 4; Length 247;
Best Local Similarity 34.9%; Pred. No. 3.4e+02;
RESULT 728
ID ABB72363 standard; protein; 247 AA.
DE Murine protein isolated from skin cells SEQ ID NO: 687.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 12.3%; Score 57; DB 5; Length 247;
Best Local Similarity 34.9%; Pred. No. 3.4e+02;
RESULT 729
ID ABP65038 standard; protein; 247 AA.
DE Mouse membrane spanning 4-domain family, subfamily A 6D protein.
PN WO200262946-A2.
PD 15-AUG-2002.
PA (UYDU-) UNIV DUKE.
Query Match 12.3%; Score 57; DB 5; Length 247;
Best Local Similarity 34.9%; Pred. No. 3.4e+02;
RESULT 730
ID ADM74700 standard; protein; 248 AA.
DE Fusarium oxysporum trypsinogen-like mutant protein - S193A.
PN WO2004029202-A2.

PD 08-APR-2004.
PA (NOVO) NOVOZYMES BIOTECH INC.
Query Match 12.3%; Score 57; DB 8; Length 248;
Best Local Similarity 21.2%; Pred. No. 3.4e+02;
RESULT 731
ID ADM74704 standard; protein; 248 AA.
DE Fusarium oxysporum trypsinogen-like mutant protein - N223S.
PN WO2004029202-A2.
PD 08-APR-2004.
PA (NOVO) NOVOZYMES BIOTECH INC.
Query Match 12.3%; Score 57; DB 8; Length 248;
Best Local Similarity 21.2%; Pred. No. 3.4e+02;
RESULT 732
ID AAU67511 standard; protein; 269 AA.
DE Propionibacterium acnes immunogenic protein #28407.
PN WO20010181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 12.3%; Score 57; DB 4; Length 269;
Best Local Similarity 26.1%; Pred. No. 3.8e+02;
RESULT 733
ID ABM64030 standard; protein; 269 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #28706.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 12.3%; Score 57; DB 6; Length 269;
Best Local Similarity 26.1%; Pred. No. 3.8e+02;
RESULT 734
ID ABM64811 standard; protein; 278 AA.
DE Propionibacterium acnes immunogenic polypeptide #29487.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 12.3%; Score 57; DB 6; Length 278;
Best Local Similarity 26.1%; Pred. No. 4e+02;
RESULT 735
ID ABU23654 standard; protein; 302 AA.
DE Protein encoded by Prokaryotic essential gene #9181.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.3%; Score 57; DB 6; Length 302;
Best Local Similarity 41.7%; Pred. No. 4.5e+02;
RESULT 736
ID ADC94298 standard; protein; 308 AA.
DE E. faecium protein sequence SEQ ID 3925.
PN US683275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.3%; Score 57; DB 7; Length 308;
Best Local Similarity 31.9%; Pred. No. 4.6e+02;
RESULT 737
ID ABU44043 standard; protein; 386 AA.
DE Protein encoded by Prokaryotic essential gene #29570.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.3%; Score 57; DB 6; Length 386;
Best Local Similarity 30.3%; Pred. No. 6.3e+02;
RESULT 738
ID AAU30690 standard; protein; 406 AA.
DE Novel human secreted protein #1181.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.3%; Score 57; DB 4; Length 406;
Best Local Similarity 37.2%; Pred. No. 6.8e+02;
RESULT 739
ID ABG13336 standard; protein; 477 AA.
DE Novel human diagnostic protein #13327.
PN WO200175067-A2.
PD 11-OCT-2001.

PA (HYSE-) HYSEQ INC.
Query Match 12.3%; Score 57; DB 4; Length 477;
Best Local Similarity 29.3%; Pred. No. 8.5e+02;
RESULT 740
ID ADA89720 standard; protein; 501 AA.
DE Staphylococcus aureus antigenic protein #259.
PN WO2003011899-A2.
PD 13-FEB-2003.
PA (UYSH-) UNIV SHEFFIELD.
PA (BIOS-) BIOSYNEXUS INC.
Query Match 12.3%; Score 57; DB 6; Length 501;
Best Local Similarity 30.0%; Pred. No. 9.1e+02;
RESULT 741
ID ADP98896 standard; protein; 589 AA.
DE C. albicans specific gene, orf6.6204, protein sequence.
PN WO2004056965-A2.
PD 08-JUL-2004.
PA (ELIT-) ELITRA PHARM INC.
PA (ELIT-) ELITRA CANADA LTD.
Query Match 12.3%; Score 57; DB 8; Length 589;
Best Local Similarity 36.4%; Pred. No. 1.1e+03;
RESULT 742
ID ABB60490 standard; protein; 614 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 8262.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NV.
Query Match 12.3%; Score 57; DB 4; Length 614;
Best Local Similarity 28.6%; Pred. No. 1.2e+03;
RESULT 743
ID ADA89583 standard; protein; 645 AA.
DE Staphylococcus aureus antigenic protein #122.
PN WO2003011899-A2.
PD 13-FEB-2003.
PA (UYSH-) UNIV SHEFFIELD.
PA (BIOS-) BIOSYNEXUS INC.
Query Match 12.3%; Score 57; DB 6; Length 645;
Best Local Similarity 30.0%; Pred. No. 1.3e+03;
RESULT 744
ID ABJ19106 standard; protein; 645 AA.
DE Pathogen specific antigen related staphylococcal protein SEQ ID NO 414.
PN WO200259148-A2.
PD 01-AUG-2002.
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
Query Match 12.3%; Score 57; DB 6; Length 645;
Best Local Similarity 30.0%; Pred. No. 1.3e+03;
RESULT 745
ID ABU42370 standard; protein; 645 AA.
DE Protein encoded by Prokaryotic essential gene #27897.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.3%; Score 57; DB 6; Length 645;
Best Local Similarity 30.0%; Pred. No. 1.3e+03;
RESULT 746
ID ABM71345 standard; protein; 645 AA.
DE Staphylococcus aureus protein #585.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 12.3%; Score 57; DB 6; Length 645;
Best Local Similarity 30.0%; Pred. No. 1.3e+03;
RESULT 747
ID ABP56879 standard; protein; 654 AA.
DE Staphylococcus epidermidis KrkN protein SEQ ID NO:10.
PN WO2002102829-A2.
PD 27-DEC-2002.
PA (INHI-) INHIBITEX INC.
PA (QUEE-) QUEEN ELIZABETH COLLEGE DUBLIN.
PA (UYPA-) UNIV PAVIA.
Query Match 12.3%; Score 57; DB 6; Length 654;
Best Local Similarity 30.0%; Pred. No. 1.3e+03;
RESULT 748

ID ABP73294 standard; protein; 821 AA.
DE Candida albicans essential protein SEQ ID NO 7131.
PN WO200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.3%; Score 57; DB 5; Length 821;
Best Local Similarity 25.0%; Pred. No. 1.8e+03;
RESULT 749
ID ABO23608 standard; protein; 861 AA.
DE Plasmodium falciparum outlier protein #5.
PN US2003039963-A1.
PD 27-FEB-2003.
PA (BRAH/) BRAHMACHARI S K.
PA (RAMA/) RAMACHANDRAN S.
PA (NAND/) NANDI T.
PA (BHIM/) BHIMARAO C.
Query Match 12.3%; Score 57; DB 7; Length 861;
Best Local Similarity 32.0%; Pred. No. 1.9e+03;
RESULT 750
ID AAE24015 standard; protein; 886 AA.
DE Escherichia coli stcE protein encoded by p0157 plasmid DNA.
PN WO200234918-A2.
PD 02-MAY-2002.
PA (WISC) WISCONSIN ALUMNI RES FOUND.
Query Match 12.3%; Score 57; DB 5; Length 886;
Best Local Similarity 25.7%; Pred. No. 2e+03;
RESULT 751
ID ABU50381 standard; protein; 1070 AA.
DE Protein encoded by Prokaryotic essential gene #35908.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.3%; Score 57; DB 6; Length 1070;
Best Local Similarity 23.4%; Pred. No. 2.6e+03;
RESULT 752
ID AAY00891 standard; protein; 1088 AA.
DE Isoleucyl-tRNA synthetase protein sequence.
PN US5885815-A.
PD 23-MAR-1999.
PA (CUBI-) CUBIST PHARM INC.
Query Match 12.3%; Score 57; DB 2; Length 1088;
Best Local Similarity 25.0%; Pred. No. 2.7e+03;
RESULT 753
ID AAY00892 standard; protein; 1088 AA.
DE Isoleucyl-tRNA synthetase protein sequence.
PN US5885815-A.
PD 23-MAR-1999.
PA (CUBI-) CUBIST PHARM INC.
Query Match 12.3%; Score 57; DB 2; Length 1088;
Best Local Similarity 25.0%; Pred. No. 2.7e+03;
RESULT 754
ID ABP73361 standard; protein; 1088 AA.
DE Candida albicans essential protein SEQ ID NO 7198.
PN WO200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.3%; Score 57; DB 5; Length 1088;
Best Local Similarity 25.0%; Pred. No. 2.7e+03;
RESULT 755
ID ADB82787 standard; protein; 1222 AA.
DE Human protein sequence useful for the treatment of cancer (SeqID 1568).
PN WO2003050236-A2.
PD 19-JUN-2003.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 12.3%; Score 57; DB 7; Length 1222;
Best Local Similarity 31.9%; Pred. No. 3.2e+03;
RESULT 756
ID ADI26360 standard; protein; 2109 AA.
DE Aspergillus parasiticus polyketide synthetase SEQ ID NO:12.
PN WO2004005522-A2.
PD 15-JAN-2004.
PA (BADI) BASF AG.

Query Match 12.3%; Score 57; DB 8; Length 2109;
Best Local Similarity 19.1%; Pred. No. 6.8e+03;
RESULT 757
ID ABB52855 standard; protein; 2732 AA.
DE Escherichia coli polypeptide SEQ ID NO 1119.
PN WO200166572-A2.
PD 13-SEP-2001.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
Query Match 12.3%; Score 57; DB 4; Length 2732;
Best Local Similarity 30.3%; Pred. No. 9.8e+03;
RESULT 758
ID ADI16953 standard; protein; 2802 AA.
DE Chicken NOVX protein homologue SeqID 490.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 12.3%; Score 57; DB 5; Length 2802;
Best Local Similarity 31.5%; Pred. No. 1e+04;
RESULT 759
ID ABG97576 standard; protein; 2834 AA.
DE Haemagglutinin-like protein encoded by E. coli CFT073 ORF1.
PN WO200259320-A2.
PD 01-AUG-2002.
PA (WISC) WISCONSIN ALUMNI RES FOUND.
Query Match 12.3%; Score 57; DB 5; Length 2834;
Best Local Similarity 30.3%; Pred. No. 1e+04;
RESULT 760
ID ADH80652 standard; protein; 2834 AA.
DE Escherichia coli CFT073 genome contig associated protein #1.
PN US2003165870-A1.
PD 04-SEP-2003.
PA (BLAT/) BLATTNER F R.
PA (WELC/) WELCH R A.
PA (BURL/) BURLAND V D.
Query Match 12.3%; Score 57; DB 7; Length 2834;
Best Local Similarity 30.3%; Pred. No. 1e+04;
RESULT 761
ID AAM94981 standard; protein; 53 AA.
DE Human reproductive system related antigen SEQ ID NO: 3639.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.2%; Score 56.5; DB 4; Length 53;
Best Local Similarity 34.2%; Pred. No. 45;
RESULT 762
ID ABB95689 standard; protein; 53 AA.
DE Human testicular antigen SEQ ID NO: 1073.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.2%; Score 56.5; DB 4; Length 53;
Best Local Similarity 34.2%; Pred. No. 45;
RESULT 763
ID AAG10323 standard; protein; 208 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 8594.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 12.2%; Score 56.5; DB 3; Length 208;
Best Local Similarity 26.7%; Pred. No. 3e+02;
RESULT 764
ID AAG10322 standard; protein; 212 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 8593.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 12.2%; Score 56.5; DB 3; Length 212;
Best Local Similarity 26.7%; Pred. No. 3.1e+02;
RESULT 765
ID AAG57749 standard; protein; 224 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 74457.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 12.2%; Score 56.5; DB 3; Length 224;
Best Local Similarity 29.5%; Pred. No. 3.4e+02;

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RESULT 766
ID AAB19097 standard; protein; 254 AA.
DE Protein encoded by reporter gene YLR194C from protein kinase C pathway.
PN WO200058520-A1.
PD 05-OCT-2000.
PA (ROSE-) ROSETTA INPHARMATICS INC.
Query Match 12.2%; Score 56.5; DB 3; Length 254;
Best Local Similarity 29.3%; Pred. No. 4e+02;
RESULT 767
ID ABM68936 standard; protein; 286 AA.
DE Phototaxis luminescens protein sequence #2033.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP ) INST PASTEUR.
PA (CNRS ) CNRS CENT NAT RECH SCI.
Query Match 12.2%; Score 56.5; DB 6; Length 286;
Best Local Similarity 19.1%; Pred. No. 4.8e+02;
RESULT 768
ID AAO17677 standard; protein; 296 AA.
DE B tropicalis allergen Biot 3 polymorphic variant protein SEQ ID NO: 39.
PN WO200230968-A1.
PD 18-APR-2002.
PA (JYST-) UNIV SINGAPORE NAT.
Query Match 12.2%; Score 56.5; DB 5; Length 296;
Best Local Similarity 20.9%; Pred. No. 5e+02;
RESULT 769
ID AAG23018 standard; protein; 329 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26168.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 12.2%; Score 56.5; DB 3; Length 329;
Best Local Similarity 25.5%; Pred. No. 5.8e+02;
RESULT 770
ID AAG49855 standard; protein; 329 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63114.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 12.2%; Score 56.5; DB 3; Length 329;
Best Local Similarity 25.5%; Pred. No. 5.8e+02;
RESULT 771
ID ADN72753 standard; protein; 329 AA.
DE Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 648.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDISEIGN NV.
Query Match 12.2%; Score 56.5; DB 8; Length 329;
Best Local Similarity 25.5%; Pred. No. 5.8e+02;
RESULT 772
ID ADB31809 standard; protein; 333 AA.
DE Plant (A. thaliana) transcription factor polypeptide #21.
PN US2003101481-A1.
PD 29-MAY-2003.
PA (ZHAN/) ZHANG J.
PA (FROM/) FROMM M.
PA (HEAR/) HEARD J.
PA (RIEC/) RIECHMANN J L.
PA (ADAM/) ADAM L.
PA (BROU/) BROUN P.
PA (FINE/) PINEDA O.
PA (REUB/) REUBER L.
PA (KEDD/) KEDDIE J.
PA (YUGG/) YU G.
PA (JIAN/) JIANG C.
Query Match 12.2%; Score 56.5; DB 7; Length 333;
Best Local Similarity 28.4%; Pred. No. 5.9e+02;
RESULT 773
ID AAE30045 standard; protein; 334 AA.
DE Arabidopsis thaliana G661 transcription factor protein.
PN WO200274917-A2.
PD 26-SEP-2002.
PA (MENDE-) MENDEL BIOTECHNOLOGY INC.
Query Match 12.2%; Score 56.5; DB 6; Length 334;
Best Local Similarity 28.4%; Pred. No. 5.9e+02;
RESULT 774
ID ADJ50409 standard; protein; 334 AA.
DE Oil-associated gene related protein #1909.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (SAVA/) RAVANELLO M.
PA (RAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match 12.2%; Score 56.5; DB 8; Length 334;
Best Local Similarity 28.4%; Pred. No. 5.9e+02;
RESULT 775
ID ADO02021 standard; protein; 334 AA.
DE Thalecress transcription factor protein #217.
PN US2004045049-A1.
PD 04-MAR-2004.
PA (ZHAN/) ZHANG J.
PA (FROM/) FROMM M E.
PA (HEAR/) HEARD J E.
PA (RIEC/) RIECHMANN J L.
PA (ADAM/) ADAM L J.
PA (BROU/) BROUN P E.
PA (FINE/) PINEDA O.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J S.
PA (YUGG/) YU G.
PA (JIAN/) JIANG C.
PA (SAVA/) SAWAHA R S.
PA (PILG/) PILGRIM M L.
PA (CREE/) CREELMAN R A.
PA (DUBE/) DUBELL A N.
PA (RATC/) RATCLIFFE O.
PA (KUMI/) KUMIMOTO R.
PA (SHER/) SHERMAN B K.
Query Match 12.2%; Score 56.5; DB 8; Length 334;
Best Local Similarity 28.4%; Pred. No. 5.9e+02;
RESULT 776
ID AAG04826 standard; protein; 358 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 999.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 12.2%; Score 56.5; DB 3; Length 358;
Best Local Similarity 29.5%; Pred. No. 6.5e+02;
RESULT 777
ID AAG61479 standard; protein; 358 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 79746.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 12.2%; Score 56.5; DB 3; Length 358;
Best Local Similarity 29.5%; Pred. No. 6.5e+02;
RESULT 778
ID AAU30389 standard; protein; 379 AA.
DE Novel human secreted protein #880.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.2%; Score 56.5; DB 4; Length 379;
Best Local Similarity 29.0%; Pred. No. 7.1e+02;
RESULT 779
ID AAU34289 standard; protein; 444 AA.
DE Staphylococcus aureus cellular proliferation protein #565.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.2%; Score 56.5; DB 4; Length 444;
Best Local Similarity 25.3%; Pred. No. 8.8e+02;
RESULT 780
ID AAU37188 standard; protein; 452 AA.
DE Staphylococcus aureus cellular proliferation protein #1358.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
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Query Match      12.2%; Score 56.5; DB 4; Length 452;
Best Local Similarity 25.3%; Pred. No. 9.1e+02;
RESULT 781
ID ABW73373 standard; protein; 452 AA.
DE Staphylococcus aureus protein #2613.
FN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.

Query Match      12.2%; Score 56.5; DB 6; Length 452;
Best Local Similarity 25.3%; Pred. No. 9.1e+02;
RESULT 782
ID ADA33236 standard; protein; 459 AA.
DE Acinetobacter baumannii protein #397.
FN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.

Query Match      12.2%; Score 56.5; DB 6; Length 459;
Best Local Similarity 29.6%; Pred. No. 9.2e+02;
RESULT 783
ID ABU45293 standard; protein; 493 AA.
DE Protein encoded by Prokaryotic essential gene #30820.
FN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.

Query Match      12.2%; Score 56.5; DB 6; Length 493;
Best Local Similarity 30.2%; Pred. No. 1e+03;
RESULT 784
ID ABU48125 standard; protein; 500 AA.
DE Protein encoded by Prokaryotic essential gene #33652.
FN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.

Query Match      12.2%; Score 56.5; DB 6; Length 500;
Best Local Similarity 30.2%; Pred. No. 1e+03;
RESULT 785
ID ABU47339 standard; protein; 500 AA.
DE Protein encoded by Prokaryotic essential gene #32866.
FN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.

Query Match      12.2%; Score 56.5; DB 6; Length 500;
Best Local Similarity 30.2%; Pred. No. 1e+03;
RESULT 786
ID AD063043 standard; protein; 538 AA.
DE Transcription factor G2546, SEQ ID 1510.
FN WO2004031349-A2.
PD 15-APR-2004.
PA (MEND-) MENDEL BIOTECHNOLOGY INC.

Query Match      12.2%; Score 56.5; DB 8; Length 538;
Best Local Similarity 20.3%; Pred. No. 1.2e+03;
RESULT 787
ID ABG93227 standard; protein; 583 AA.
DE C. albicans BAX-associated protein fragment SEQ ID 412.
FN WO200264766-A2.
PD 22-AUG-2002.
PA (JANC-) JANSSEN PHARM NV.

Query Match      12.2%; Score 56.5; DB 5; Length 583;
Best Local Similarity 29.3%; Pred. No. 1.3e+03;
RESULT 788
ID AAG79971 standard; protein; 636 AA.
DE Soybean granule-bound starch synthase.
FN CA2384605-A1.
PD 03-NOV-2002.
PA (DUPO-) DU PONT DE NEMOURS & CO E I.

Query Match      12.2%; Score 56.5; DB 6; Length 636;
Best Local Similarity 24.5%; Pred. No. 1.5e+03;
RESULT 789
ID ADR87948 standard; protein; 717 AA.
DE Enterococcus faecalis polypeptide #2428.
FN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PD (BUSH/) BUSH D.

Query Match      12.2%; Score 56.5; DB 7; Length 717;
Best Local Similarity 25.4%; Pred. No. 1.7e+03;
RESULT 790
ID AAW80322 standard; protein; 746 AA.
DE Bacillus thuringiensis VIP3A(c) polypeptide.
FN WO9844137-A2.
PD 08-OCT-1998.
PA (NOVS) NOVARTIS AG.

Query Match      12.2%; Score 56.5; DB 2; Length 746;
Best Local Similarity 39.2%; Pred. No. 1.8e+03;
RESULT 791
ID ADA36363 standard; protein; 759 AA.
DE Acinetobacter baumannii protein #3524.
FN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.

Query Match      12.2%; Score 56.5; DB 6; Length 759;
Best Local Similarity 36.8%; Pred. No. 1.9e+03;
RESULT 792
ID ADN08762 standard; protein; 788 AA.
DE B. thuringiensis vip3A-C fusion protein SEQ ID NO.11.
FN WO2003075655-A2.
PD 18-SEP-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.

Query Match      12.2%; Score 56.5; DB 7; Length 788;
Best Local Similarity 39.2%; Pred. No. 2e+03;
RESULT 793
ID AAR91244 standard; protein; 789 AA.
DE B. thuringiensis VIP3A(b) insecticidal protein.
FN WO9610083-A1.
PD 04-APR-1996.
PA (CIBA) CIBA GEIGY AG.

Query Match      12.2%; Score 56.5; DB 2; Length 789;
Best Local Similarity 39.2%; Pred. No. 2e+03;
RESULT 794
ID AAR91243 standard; protein; 789 AA.
DE B. thuringiensis VIP3A(a) insecticidal protein.
FN WO9610083-A1.
PD 04-APR-1996.
PA (CIBA) CIBA GEIGY AG.

Query Match      12.2%; Score 56.5; DB 2; Length 789;
Best Local Similarity 39.2%; Pred. No. 2e+03;
RESULT 795
ID AAW19515 standard; protein; 789 AA.
DE B. cereus VIP3A(b) protein sequence.
FN WO9726339-A1.
PD 24-JUL-1997.
PA (NOVS) NOVARTIS AG.

Query Match      12.2%; Score 56.5; DB 2; Length 789;
Best Local Similarity 39.2%; Pred. No. 2e+03;
RESULT 796
ID AAW19514 standard; protein; 789 AA.
DE B. cereus VIP3A(a) protein sequence.
FN WO9726339-A1.
PD 24-JUL-1997.
PA (NOVS) NOVARTIS AG.

Query Match      12.2%; Score 56.5; DB 2; Length 789;
Best Local Similarity 39.2%; Pred. No. 2e+03;
RESULT 797
ID AAW80321 standard; protein; 789 AA.
DE Bacillus thuringiensis VIP3A(b) polypeptide.
FN WO9844137-A2.
PD 08-OCT-1998.
PA (NOVS) NOVARTIS AG.

Query Match      12.2%; Score 56.5; DB 2; Length 789;
Best Local Similarity 39.2%; Pred. No. 2e+03;
RESULT 798
ID AAW80320 standard; protein; 789 AA.
DE Bacillus thuringiensis VIP3A(a) polypeptide.
FN WO9844137-A2.
PD 08-OCT-1998.
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PA (NOVS) NOVARTIS AG.
Query Match 12.2%; Score 56.5; DB 2; Length 789;
Best Local Similarity 39.2%; Pred. No. 2e+03;
RESULT 799
ID AAW60217 standard; protein; 789 AA.
DE Bacillus thuringiensis Javelin 1990 insecticidal toxin.
PN WO9818932-A2.
PD 07-MAY-1998.
PA (MYCO) MYCOGEN CORP.
Query Match 12.2%; Score 56.5; DB 2; Length 789;
Best Local Similarity 39.2%; Pred. No. 2e+03;
RESULT 800
ID AAW46726 standard; protein; 789 AA.
DE Native vegetative insecticidal protein 3A(b).
PN WO9746105-A1.
PD 11-DEC-1997.
PA (NOVS) NOVARTIS AG.
Query Match 12.2%; Score 56.5; DB 2; Length 789;
Best Local Similarity 39.2%; Pred. No. 2e+03;
RESULT 801
ID AAW46725 standard; protein; 789 AA.
DE Vegetative insecticidal protein 3(a) (VIP3A(a)) of Bacillus cereus.
PN WO9746105-A1.
PD 11-DEC-1997.
PA (NOVS) NOVARTIS AG.
Query Match 12.2%; Score 56.5; DB 2; Length 789;
Best Local Similarity 39.2%; Pred. No. 2e+03;
RESULT 802
ID AAW46860 standard; protein; 789 AA.
DE Bacillus thuringiensis toxin designated 11B(a).
PN WO9800546-A2.
PD 08-JAN-1998.
PA (MYCO) MYCOGEN CORP.
Query Match 12.2%; Score 56.5; DB 2; Length 789;
Best Local Similarity 39.2%; Pred. No. 2e+03;
RESULT 803
ID AAW46868 standard; protein; 789 AA.
DE Bacillus thuringiensis toxin designated 213E5(a).
PN WO9800546-A2.
PD 08-JAN-1998.
PA (MYCO) MYCOGEN CORP.
Query Match 12.2%; Score 56.5; DB 2; Length 789;
Best Local Similarity 39.2%; Pred. No. 2e+03;
RESULT 804
ID AAW46869 standard; protein; 789 AA.
DE Bacillus thuringiensis toxin designated 218G2(a).
PN WO9800546-A2.
PD 08-JAN-1998.
PA (MYCO) MYCOGEN CORP.
Query Match 12.2%; Score 56.5; DB 2; Length 789;
Best Local Similarity 39.2%; Pred. No. 2e+03;
RESULT 805
ID AAW46861 standard; protein; 789 AA.
DE Bacillus thuringiensis toxin designated 31G1(b).
PN WO9800546-A2.
PD 08-JAN-1998.
PA (MYCO) MYCOGEN CORP.
Query Match 12.2%; Score 56.5; DB 2; Length 789;
Best Local Similarity 39.2%; Pred. No. 2e+03;
RESULT 806
ID AAY24971 standard; protein; 789 AA.
DE Bacillus thuringiensis toxin 213E5(a).
PN WO9933991-A2.
PD 08-JUL-1999.
PA (MYCO) MYCOGEN CORP.
Query Match 12.2%; Score 56.5; DB 2; Length 789;
Best Local Similarity 39.2%; Pred. No. 2e+03;
RESULT 807
ID AAY24972 standard; protein; 789 AA.
DE Bacillus thuringiensis toxin 218G2(a).
PN WO9933991-A2.
PD 08-JUL-1999.
PA (NOVS) NOVARTIS AG.
Query Match 12.2%; Score 56.5; DB 2; Length 789;
Best Local Similarity 39.2%; Pred. No. 2e+03;
RESULT 798
ID AAY24964 standard; protein; 789 AA.
DE Bacillus thuringiensis toxin 31G1(b).
PN WO9933991-A2.
PD 08-JUL-1999.
PA (MYCO) MYCOGEN CORP.
Query Match 12.2%; Score 56.5; DB 2; Length 789;
Best Local Similarity 39.2%; Pred. No. 2e+03;
RESULT 799
ID AAY24963 standard; protein; 789 AA.
DE Bacillus thuringiensis toxin 11B(a).
PN WO9933991-A2.
PD 08-JUL-1999.
PA (MYCO) MYCOGEN CORP.
Query Match 12.2%; Score 56.5; DB 2; Length 789;
Best Local Similarity 39.2%; Pred. No. 2e+03;
RESULT 800
ID AAY24963 standard; protein; 789 AA.
DE Bacillus thuringiensis toxin 11B(a).
PN WO9933991-A2.
PD 08-JUL-1999.
PA (MYCO) MYCOGEN CORP.
Query Match 12.2%; Score 56.5; DB 2; Length 789;
Best Local Similarity 39.2%; Pred. No. 2e+03;
RESULT 801
ID ABB82566 standard; protein; 789 AA.
DE B. thuringiensis native Vip3A polypeptide.
PN WO200278437-A2.
PD 10-OCT-2002.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 12.2%; Score 56.5; DB 6; Length 789;
Best Local Similarity 39.2%; Pred. No. 2e+03;
RESULT 811
ID ADN08756 standard; protein; 789 AA.
DE B. thuringiensis vip3A SEQ ID NO:5.
PN WO2003075655-A2.
PD 18-SEP-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 12.2%; Score 56.5; DB 7; Length 789;
Best Local Similarity 39.2%; Pred. No. 2e+03;
RESULT 812
ID ADN61600 standard; protein; 789 AA.
DE VIP3A toxin protein amino acid sequence SEQ ID NO:8.
PN WO200403986-A1.
PD 13-MAY-2004.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 12.2%; Score 56.5; DB 8; Length 789;
Best Local Similarity 39.2%; Pred. No. 2e+03;
RESULT 813
ID AAW60215 standard; protein; 790 AA.
DE Bacillus thuringiensis insecticidal 36A toxin.
PN WO9818932-A2.
PD 07-MAY-1998.
PA (MYCO) MYCOGEN CORP.
Query Match 12.2%; Score 56.5; DB 2; Length 790;
Best Local Similarity 39.2%; Pred. No. 2e+03;
RESULT 814
ID AAY59275 standard; protein; 790 AA.
DE Toxin from B. thuringiensis strain Javelin 1990.
PN WO9957282-A2.
PD 11-NOV-1999.
PA (MYCO) MYCOGEN CORP.
Query Match 12.2%; Score 56.5; DB 3; Length 790;
Best Local Similarity 39.2%; Pred. No. 2e+03;
RESULT 815
ID ADG88492 standard; protein; 790 AA.
DE Bacillus thuringiensis strain Javelin 1990 toxin protein.
PN US6603063-B1.
PD 05-AUG-2003.
PA (MYCO) MYCOGEN CORP.
Query Match 12.2%; Score 56.5; DB 8; Length 790;
Best Local Similarity 39.2%; Pred. No. 2e+03;
RESULT 816
ID AAR91261 standard; protein; 809 AA.
DE VIP3A(a) synthetic:native protein fusion.
PN WO9610083-A1.
PD 04-APR-1996.
PA (CIBA) CIBA GEIGY AG.

Query Match
Best Local Similarity 12.2%; Score 56.5; DB 2; Length 809;
RESULT 817
ID AAM19521 standard; protein; 809 AA.
DE B. cereus VIP3A(a) synthetic:native fusion protein.
PN WO9726339-A1.
PD 24-JUL-1997.
PA (NOVS) NOVARTIS AG.
Query Match
Best Local Similarity 12.2%; Score 56.5; DB 2; Length 809;
RESULT 818
ID AAM46732 standard; protein; 809 AA.
DE Maize optimised VIP3A(a)/native VIP3A(a) fusion protein.
PN WO9746105-A1.
PD 11-DEC-1997.
PA (NOVS) NOVARTIS AG.
Query Match
Best Local Similarity 12.2%; Score 56.5; DB 2; Length 809;
RESULT 819
ID ABB08523 standard; protein; 838 AA.
DE Amino acid sequence of bovine liver GPI-PLD.
PN WO200202756-A2.
PD 10-JAN-2002.
PA (UNLO) UNIV COLLEGE LONDON.
Query Match
Best Local Similarity 12.2%; Score 56.5; DB 5; Length 838;
RESULT 820
ID ABU41082 standard; protein; 867 AA.
DE Protein encoded by Prokaryotic essential gene #26609.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 12.2%; Score 56.5; DB 6; Length 867;
RESULT 821
ID ADF04483 standard; protein; 870 AA.
DE Bacterial polypeptide #596.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 12.2%; Score 56.5; DB 7; Length 870;
RESULT 822
ID ADF05500 standard; protein; 872 AA.
DE Bacterial polypeptide #1613.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 12.2%; Score 56.5; DB 7; Length 872;
RESULT 823
ID ABU40731 standard; protein; 873 AA.
DE Protein encoded by Prokaryotic essential gene #26258.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 12.2%; Score 56.5; DB 6; Length 873;
RESULT 824
ID ABB61328 standard; protein; 1409 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 10776.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 12.2%; Score 56.5; DB 4; Length 1409;
RESULT 825
ID AB53041 standard; protein; 1428 AA.
DE Protein sequence #SEQ ID 947.
PN EPI258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match 12.2%; Score 56.5; DB 6; Length 1428;

Best Local Similarity 34.4%; Pred. No. 4.5e+03;
RESULT 826
ID ADK62192 standard; protein; 1428 AA.
DE Disease treating protein complex-derived protein #222.
PN EPI338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match
Best Local Similarity 12.2%; Score 56.5; DB 7; Length 1428;
RESULT 827
ID ABP47797 standard; protein; 1429 AA.
DE Yeast DNA topoisomerase.
PN WO200244112-A1.
PD 06-JUN-2002.
PA (TOSU-) TOYO SUISAN KAISHA LTD.
Query Match
Best Local Similarity 12.2%; Score 56.5; DB 5; Length 1429;
RESULT 828
ID AAB83976 standard; protein; 1434 AA.
DE Amino acid sequence of a type I polyketide synthase.
PN WO200140497-A2.
PD 07-JUN-2001.
PA (AVET) AVENTIS PHARMA SA.
Query Match
Best Local Similarity 12.2%; Score 56.5; DB 4; Length 1434;
RESULT 829
ID ABG08982 standard; protein; 1447 AA.
DE Novel human diagnostic protein #8973.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 12.2%; Score 56.5; DB 4; Length 1447;
RESULT 830
ID ABG05477 standard; protein; 1859 AA.
DE Novel human diagnostic protein #5468.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 12.2%; Score 56.5; DB 4; Length 1859;
RESULT 831
ID AAU85008 standard; protein; 5546 AA.
DE Human melanocyte differentiation antigens savine.
PN WO200190197-A1.
PD 29-NOV-2001.
PA (AUSU) UNIV AUSTRALIAN NAT.
Query Match
Best Local Similarity 12.2%; Score 56.5; DB 5; Length 5546;
RESULT 832
ID AAE10129 standard; protein; 11096 AA.
DE Streptomyces noursei nystatin gene, NysC.
PN WO200159126-A2.
PD 16-AUG-2001.
PA (UVNO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.
PA (SNTF) SINTEF STIFTELSEN IND TEK FORSK.
PA (ALPH-) ALPHARMA AS.
PA (SINV-) SINVENT AS.
PA (DZIE/) DZIEGLEWSKA H.
PA (ZOTC/) ZOTCHEV S B.
PA (SEKU/) SEKUROVA O N.
PA (EJAE/) FJAERVIK E.
PA (BRAU/) BRAUTASET T.
PA (STRO/) STROM A R.
PA (VALL/) VALLA S.
Query Match
Best Local Similarity 12.2%; Score 56.5; DB 4; Length 11096;
RESULT 833
ID AAU63229 standard; protein; 91 AA.
DE Propionibacterium acnes immunogenic protein #24125.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.

Query Match 12.1%; Score 56; DB 4; Length 91;
Best Local Similarity 36.4%; Pred. No. 1.1e+02;
RESULT 834
ID ABM59748 standard; protein; 91 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #24424.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 12.1%; Score 56; DB 6; Length 91;
Best Local Similarity 36.4%; Pred. No. 1.1e+02;
RESULT 835
ID ADHI2900 standard; protein; 113 AA.
DE Francisella tularensis immunogenic protein 81, SEQ ID NO:81.
PN WO2004003009-A2.
PD 08-JAN-2004.
PA (MINA) UK SEC FOR DEFENCE.
Query Match 12.1%; Score 56; DB 8; Length 113;
Best Local Similarity 25.6%; Pred. No. 1.5e+02;
RESULT 836
ID AAY86021 standard; protein; 158 AA.
DE S. pneumoniae derived protein #230.
PN WO9806734-A1.
PD 19-FEB-1998.
PA (SMIX) SMITHKLINE BEECHAM CORP.
Query Match 12.1%; Score 56; DB 2; Length 158;
Best Local Similarity 21.9%; Pred. No. 2.4e+02;
RESULT 837
ID AAB09835 standard; protein; 162 AA.
DE Novel human protein (NHP) #1.
PN WO200164718-A2.
PD 07-SEP-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 12.1%; Score 56; DB 4; Length 162;
Best Local Similarity 29.9%; Pred. No. 2.5e+02;
RESULT 838
ID ADA55705 standard; protein; 169 AA.
DE Human protein, SEQ ID 3273.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 12.1%; Score 56; DB 6; Length 169;
Best Local Similarity 31.4%; Pred. No. 2.6e+02;
RESULT 839
ID ABB54209 standard; protein; 196 AA.
DE Lactococcus lactis protein ppiB.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 12.1%; Score 56; DB 5; Length 196;
Best Local Similarity 29.7%; Pred. No. 3.2e+02;
RESULT 840
ID ABB70335 standard; protein; 204 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 37797.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.1%; Score 56; DB 4; Length 204;
Best Local Similarity 32.4%; Pred. No. 3.4e+02;
RESULT 841
ID ABB97366 standard; protein; 217 AA.
DE Novel human protein SEQ ID NO: 634.
PN WO200222660-A2.
PD 21-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 12.1%; Score 56; DB 5; Length 217;
Best Local Similarity 29.5%; Pred. No. 3.7e+02;
RESULT 842
ID ADB10556 standard; protein; 243 AA.
DE Alloiococcus otitis antigenic protein SEQ ID NO:4504.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.

Query Match 12.1%; Score 56; DB 6; Length 243;
Best Local Similarity 27.8%; Pred. No. 4.4e+02;
RESULT 843
ID ADM74702 standard; protein; 248 AA.
DE Fusarium oxysporum trypsinogen-like mutant protein - Q201M.
PN WO2004029202-A2.
PD 08-APR-2004.
PA (NOVO) NOVOZYMES BIOTECH INC.
Query Match 12.1%; Score 56; DB 8; Length 248;
Best Local Similarity 22.4%; Pred. No. 4.5e+02;
RESULT 844
ID ADB10554 standard; protein; 249 AA.
DE Alloiococcus otitis antigenic protein SEQ ID NO:4506.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Query Match 12.1%; Score 56; DB 6; Length 249;
Best Local Similarity 27.8%; Pred. No. 4.5e+02;
RESULT 845
ID ABB67829 standard; protein; 269 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 30279.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.1%; Score 56; DB 4; Length 269;
Best Local Similarity 25.3%; Pred. No. 5e+02;
RESULT 846
ID AAM93507 standard; protein; 275 AA.
DE Human polypeptide, SEQ ID NO: 3223.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 12.1%; Score 56; DB 4; Length 275;
Best Local Similarity 31.2%; Pred. No. 5.2e+02;
RESULT 847
ID ADL31190 standard; protein; 275 AA.
DE Human protein encoded by a full length cDNA clone SeqID 3223.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 12.1%; Score 56; DB 8; Length 275;
Best Local Similarity 31.2%; Pred. No. 5.2e+02;
RESULT 848
ID AAE09837 standard; protein; 278 AA.
DE Novel human protein (NHP) #3.
PN WO200164718-A2.
PD 07-SEP-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 12.1%; Score 56; DB 4; Length 278;
Best Local Similarity 29.9%; Pred. No. 5.3e+02;
RESULT 849
ID AAM62774 standard; protein; 287 AA.
DE Human receptor for Fc gamma and Fc alpha, designated YB01.
PN WO9824906-A2.
PD 11-JUN-1998.
PA (SCHE) SCHERING CORP.
Query Match 12.1%; Score 56; DB 2; Length 287;
Best Local Similarity 32.1%; Pred. No. 5.5e+02;
RESULT 850
ID AAM62775 standard; protein; 287 AA.
DE Human receptor for Fc gamma and Fc alpha.
PN WO9824906-A2.
PD 11-JUN-1998.
PA (SCHE) SCHERING CORP.
Query Match 12.1%; Score 56; DB 2; Length 287;
Best Local Similarity 32.1%; Pred. No. 5.5e+02;
RESULT 851
ID AAB58453 standard; protein; 322 AA.
DE Lung cancer associated polypeptide sequence SEQ ID 791.
PN WO200055180-A2.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.

Query Match 12.1%; Score 56; DB 3; Length 322;
 Best Local Similarity 32.1%; Pred. No. 6.5e+02;
 RESULT 852
 ID ABP41696 standard; protein; 322 AA.
 DE Human ovarian antigen HVBV73, SEQ ID NO:2828.
 PN WO200200677-A1.
 PD 03-JAN-2002.
 PA (HUNA-) HUMAN GENOME SCI INC.
 Query Match 12.1%; Score 56; DB 5; Length 322;
 Best Local Similarity 32.1%; Pred. No. 6.5e+02;
 RESULT 853
 ID ABB90591 standard; protein; 323 AA.
 DE Chlamydia pneumoniae cp6890 protein, SEQ ID NO:131.
 PN WO200202606-A2.
 PD 10-JAN-2002.
 PA (CHIR-) CHIRON SPA.
 Query Match 12.1%; Score 56; DB 5; Length 323;
 Best Local Similarity 24.0%; Pred. No. 6.5e+02;
 RESULT 854
 ID AAY35219 standard; protein; 328 AA.
 DE Chlamydia pneumoniae transmembrane protein sequence.
 PN WO9927105-A2.
 PD 03-JUN-1999.
 PA (GST-) GENSET.
 Query Match 12.1%; Score 56; DB 2; Length 328;
 Best Local Similarity 24.0%; Pred. No. 6.6e+02;
 RESULT 855
 ID AAY94660 standard; protein; 351 AA.
 DE Soybean CCR4 transcription factor amino acid sequence.
 PN WO200032783-A1.
 PD 08-JUN-2000.
 PA (DUPO-) DU PONT DE NEMOURS & CO E I.
 Query Match 12.1%; Score 56; DB 3; Length 351;
 Best Local Similarity 30.0%; Pred. No. 7.3e+02;
 RESULT 856
 ID ADO07190 standard; protein; 362 AA.
 DE Saccharomyces cerevisiae asparaginase.
 PN WO2004032648-A1.
 PD 22-APR-2004.
 PA (NOVO-) NOVOZYMES AS.
 Query Match 12.1%; Score 56; DB 8; Length 362;
 Best Local Similarity 23.2%; Pred. No. 7.6e+02;
 RESULT 857
 ID ADA36572 standard; protein; 384 AA.
 DE Acinetobacter baumannii protein #3733.
 PN US6562958-B1.
 PD 13-MAY-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 12.1%; Score 56; DB 6; Length 384;
 Best Local Similarity 24.4%; Pred. No. 8.3e+02;
 RESULT 858
 ID ADH71238 standard; protein; 390 AA.
 DE Human protein of the invention NOV7k SEQ ID NO:134.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 12.1%; Score 56; DB 8; Length 390;
 Best Local Similarity 31.5%; Pred. No. 8.5e+02;
 RESULT 859
 ID ADH71234 standard; protein; 390 AA.
 DE Human protein of the invention NOV7i SEQ ID NO:130.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 12.1%; Score 56; DB 8; Length 390;
 Best Local Similarity 31.5%; Pred. No. 8.5e+02;
 RESULT 860
 ID ADO05831 standard; protein; 398 AA.
 DE Human teneurin polypeptide fragment.
 PN WO2004036213-A1.
 PD 29-APR-2004.
 PA (NOVS-) NOVARTIS FORSCHUNGSSSTIFTUNG.
 Query Match 12.1%; Score 56; DB 8; Length 398;

Best Local Similarity 31.5%; Pred. No. 8.7e+02;
 RESULT 861
 ID ADH71256 standard; protein; 400 AA.
 DE Human protein of the invention NOV7t SEQ ID NO:152.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 12.1%; Score 56; DB 8; Length 400;
 Best Local Similarity 31.5%; Pred. No. 8.8e+02;
 RESULT 862
 ID ADH71244 standard; protein; 400 AA.
 DE Human protein of the invention NOV7n SEQ ID NO:140.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 12.1%; Score 56; DB 8; Length 400;
 Best Local Similarity 31.5%; Pred. No. 8.8e+02;
 RESULT 863
 ID AAO30836 standard; protein; 401 AA.
 DE Human cell adhesion and extracellular matrix protein (CADECM)-26.
 PN WO2003047526-A2.
 PD 12-JUN-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 12.1%; Score 56; DB 7; Length 401;
 Best Local Similarity 33.3%; Pred. No. 8.8e+02;
 RESULT 864
 ID AAY20140 standard; protein; 402 AA.
 DE B. burgdorferi antigenic protein, f04A.aa BB011.
 PN WO9859071-A1.
 PD 30-DEC-1998.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (MEDI-) MEDIMMUNE INC.
 Query Match 12.1%; Score 56; DB 2; Length 402;
 Best Local Similarity 25.3%; Pred. No. 8.8e+02;
 RESULT 865
 ID ABP40527 standard; protein; 414 AA.
 DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5372.
 PN US6380370-B1.
 PD 30-APR-2002.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 12.1%; Score 56; DB 5; Length 414;
 Best Local Similarity 28.0%; Pred. No. 9.2e+02;
 RESULT 866
 ID ABU42566 standard; protein; 443 AA.
 DE Protein encoded by Prokaryotic essential gene #28093.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 12.1%; Score 56; DB 6; Length 443;
 Best Local Similarity 28.0%; Pred. No. 1e+03;
 RESULT 867
 ID AAY5925 standard; protein; 476 AA.
 DE Pseudomonas fluorescens lipase protein.
 PN JP11276172-A.
 PD 12-OCT-1999.
 PA (TANA-) TANABE SEIYAKU CO.
 Query Match 12.1%; Score 56; DB 2; Length 476;
 Best Local Similarity 30.7%; Pred. No. 1.1e+03;
 RESULT 868
 ID AAY90300 standard; protein; 476 AA.
 DE Human peptidase, HPEP-17 protein sequence.
 PN WO200042201-A2.
 PD 20-JUL-2000.
 PA (INCY-) INCYTE PHARM INC.
 Query Match 12.1%; Score 56; DB 3; Length 476;
 Best Local Similarity 33.3%; Pred. No. 1.1e+03;
 RESULT 869
 ID ASU12080 standard; protein; 476 AA.
 DE Human NOV23b 188822752 protein SEQ ID 80.
 PN WO200281625-A2.
 PD 17-OCT-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 12.1%; Score 56; DB 6; Length 476;

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Best Local Similarity 35.3%; Pred. No. 1.1e+03;
RESULT 870
ID AAB82922 standard; protein; 509 AA.
DE Human osteoregulin (mature polypeptide).
PN EPI130098-A2.
PD 05-SEP-2001.
PA (PFIZ) PFIZER PROD INC.
Query Match 12.1%; Score 56; DB 4; Length 509;
Best Local Similarity 31.2%; Pred. No. 1.2e+03;
RESULT 871
ID AAB82920 standard; protein; 525 AA.
DE Human osteoregulin.
PN EPI130098-A2.
PD 05-SEP-2001.
PA (PFIZ) PFIZER PROD INC.
Query Match 12.1%; Score 56; DB 4; Length 525;
Best Local Similarity 31.2%; Pred. No. 1.3e+03;
RESULT 872
ID AAB62689 standard; protein; 525 AA.
DE Phosphatonin polypeptide (MEPE).
PN WO200132878-A2.
PD 10-MAY-2001.
PA (UNLO) UNIV COLLEGE LONDON.
Query Match 12.1%; Score 56; DB 4; Length 525;
Best Local Similarity 31.2%; Pred. No. 1.3e+03;
RESULT 873
ID ABB08526 standard; protein; 525 AA.
DE Human phosphatonin.
PN WO200198495-A1.
PD 27-DEC-2001.
PA (TAKA) TAKEDA CHEM IND LTD.
Query Match 12.1%; Score 56; DB 5; Length 525;
Best Local Similarity 31.2%; Pred. No. 1.3e+03;
RESULT 874
ID AAE13227 standard; protein; 525 AA.
DE Human oncogenic osteomalacia-related protein-1 (OOM-1).
PN WO200172826-A2.
PD 04-OCT-2001.
PA (GENZ) GENZYME CORP.
Query Match 12.1%; Score 56; DB 5; Length 525;
Best Local Similarity 31.2%; Pred. No. 1.3e+03;
RESULT 875
ID ADF16221 standard; protein; 525 AA.
DE Human albumin fusion protein-related protein SeqID1308.
PN WO2003060071-A2.
PD 24-JUL-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (DELZ) DELTA BIOTECHNOLOGY LTD.
PA (PRIN-) PRINCIPIA PHARM CORP.
Query Match 12.1%; Score 56; DB 7; Length 525;
Best Local Similarity 31.2%; Pred. No. 1.3e+03;
RESULT 876
ID ADK72422 standard; protein; 525 AA.
DE Human 525 amino acid bone differentiation promoter protein.
PN JP2004026692-A.
PD 29-JAN-2004.
PA (TAKA) TAKEDA CHEM IND LTD.
Query Match 12.1%; Score 56; DB 8; Length 525;
Best Local Similarity 31.2%; Pred. No. 1.3e+03;
RESULT 877
ID ADH71236 standard; protein; 531 AA.
DE Human protein of the invention NOV7j SEQ ID NO:132.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.1%; Score 56; DB 8; Length 531;
Best Local Similarity 31.5%; Pred. No. 1.3e+03;
RESULT 878
ID AAB82923 standard; protein; 540 AA.
DE Human osteoregulin (mature polypeptide).
PN EPI130098-A2.
PD 05-SEP-2001.

PA (PFIZ) PFIZER PROD INC.
Query Match 12.1%; Score 56; DB 4; Length 540;
Best Local Similarity 31.2%; Pred. No. 1.3e+03;
RESULT 879
ID AAB31559 standard; protein; 549 AA.
DE Pimaricin biosynthesis associated oxidation enzyme PORF1.
PN WO200077222-A1.
PD 21-DEC-2000.
PA (STAM) DSM NV.
Query Match 12.1%; Score 56; DB 4; Length 549;
Best Local Similarity 25.6%; Pred. No. 1.4e+03;
RESULT 880
ID AAB82921 standard; protein; 556 AA.
DE Human osteoregulin.
PN EPI130098-A2.
PD 05-SEP-2001.
PA (PFIZ) PFIZER PROD INC.
Query Match 12.1%; Score 56; DB 4; Length 556;
Best Local Similarity 31.2%; Pred. No. 1.4e+03;
RESULT 881
ID ABU17761 standard; protein; 574 AA.
DE Protein encoded by Prokaryotic essential gene #3288.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.1%; Score 56; DB 6; Length 574;
Best Local Similarity 28.8%; Pred. No. 1.5e+03;
RESULT 882
ID ADH71242 standard; protein; 580 AA.
DE Human protein of the invention NOV7m SEQ ID NO:138.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.1%; Score 56; DB 8; Length 580;
Best Local Similarity 31.5%; Pred. No. 1.5e+03;
RESULT 883
ID ADH71248 standard; protein; 580 AA.
DE Human protein of the invention NOV7p SEQ ID NO:144.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.1%; Score 56; DB 8; Length 580;
Best Local Similarity 31.5%; Pred. No. 1.5e+03;
RESULT 884
ID ASU02715 standard; protein; 608 AA.
DE S. pneumoniae type 4 strain protein from coding region #2294.
PN WO200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 12.1%; Score 56; DB 6; Length 608;
Best Local Similarity 29.2%; Pred. No. 1.6e+03;
RESULT 885
ID ADK47809 standard; protein; 608 AA.
DE Streptococcus pneumoniae protein, Seq ID No 4324.
PN US6699703-B1.
PD 02-MAR-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.1%; Score 56; DB 8; Length 608;
Best Local Similarity 29.2%; Pred. No. 1.6e+03;
RESULT 886
ID AAY81508 standard; protein; 609 AA.
DE Streptococcus pneumoniae type 4 protein sequence #8.
PN WO200006737-A2.
PD 10-FEB-2000.
PA (MTCR-) MICROBIAL TECHNIQS LTD.
Query Match 12.1%; Score 56; DB 3; Length 609;
Best Local Similarity 29.2%; Pred. No. 1.6e+03;
RESULT 887
ID ABG91788 standard; protein; 622 AA.
DE Purine/pyrimidine triphosphate type nucleotidyltransferase #373.
PN WO200248331-A2.
PD 20-JUN-2002.

PA (SLOK) SLOAN KETTERING INST CANCER RES.
 Query Match 12.1%; Score 56; DB 5; Length 622;
 Best Local Similarity 23.4%; Pred. No. 1.6e+03;
 RESULT 888
 ID ADD30941 standard; protein; 631 AA.
 DE Plant yield-related protein from clone G958.
 PN WO2003013227-A2.
 PD 20-FEB-2003.
 PA (MEND-) MENDEL BIOTECHNOLOGY INC.
 Query Match 12.1%; Score 56; DB 7; Length 631;
 Best Local Similarity 24.4%; Pred. No. 1.7e+03;
 RESULT 889
 ID ADI44009 standard; protein; 631 AA.
 DE Plant transcription factor related polypeptide #1593.
 PN US2004019927-A1.
 PD 29-JAN-2004.
 PA (SHER/) SHERMAN B K.
 PA (RIEC/) RIECHMANN J L.
 PA (JIAN/) JIANG C.
 PA (HEAR/) HEARD J E.
 PA (HAAK/) HAAKE V.
 PA (CREE/) CREELMAN R A.
 PA (RATC/) RATCLIFFE O.
 PA (ADAM/) ADAM L J.
 PA (REUB/) REUBER T L.
 PA (KEDD/) KEDDIE J.
 PA (BROU/) BROUN P E.
 PA (PILG/) PILGRIM M L.
 PA (DUBE/) DUBELL A N.
 PA (PINE/) PINEDA O.
 PA (YUGG/) YU G.
 Query Match 12.1%; Score 56; DB 8; Length 631;
 Best Local Similarity 24.4%; Pred. No. 1.7e+03;
 RESULT 890
 ID ADB64241 standard; protein; 695 AA.
 DE Human protein encoded by clone DFNES20029660.
 PN EPI308459-A2.
 PD 07-MAY-2003.
 PA (HELL-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 12.1%; Score 56; DB 7; Length 695;
 Best Local Similarity 29.5%; Pred. No. 1.9e+03;
 RESULT 891
 ID ABG19897 standard; protein; 704 AA.
 DE Novel human diagnostic protein #19888.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 12.1%; Score 56; DB 4; Length 704;
 Best Local Similarity 32.8%; Pred. No. 1.9e+03;
 RESULT 892
 ID ABU40942 standard; protein; 726 AA.
 DE Protein encoded by Prokaryotic essential gene #26469.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 12.1%; Score 56; DB 6; Length 726;
 Best Local Similarity 28.2%; Pred. No. 2e+03;
 RESULT 893
 ID ADF05412 standard; protein; 747 AA.
 DE Bacterial polypeptide #1525.
 PN US6605709-B1.
 PD 12-AUG-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 12.1%; Score 56; DB 7; Length 747;
 Best Local Similarity 28.2%; Pred. No. 2.1e+03;
 RESULT 894
 ID ADI45375 standard; protein; 835 AA.
 DE Rice isoprenoid biosynthesis-associated protein #153.
 PN US2004010815-A1.
 PD 15-JAN-2004.
 PA (LANG/) LANGE B M.
 PA (GHAS/) GHASSEMIA M.

PA (BRIG/) BRIGGS S P.
 PA (COOP/) COOPER B.
 PA (GLAZ/) GLAZEBROOK J.
 PA (GOFF/) GOFF S A.
 PA (KATA/) KATAGIRI F.
 PA (KREP/) KREPS J.
 PA (MOUG/) MOUGHAMER T.
 PA (PROV/) PROVART N.
 PA (RICK/) RICKÉ D.
 PA (ZHUT/) ZHU T.
 Query Match 12.1%; Score 56; DB 8; Length 835;
 Best Local Similarity 25.3%; Pred. No. 2.5e+03;
 RESULT 895
 ID AAB74921 standard; protein; 850 AA.
 DE Pteris rapae pterisin apoptosis-inducing protein.
 PN JP2001025390-A.
 PD 30-JAN-2001.
 PA (MEIP) MEIJI MILK PROD CO LTD.
 PA (SUGI/) SUGIMURA T.
 Query Match 12.1%; Score 56; DB 4; Length 850;
 Best Local Similarity 27.0%; Pred. No. 2.5e+03;
 RESULT 896
 ID AAE09850 standard; protein; 877 AA.
 DE Novel human protein (NHP) #16.
 PN WO200164718-A2.
 PD 07-SEP-2001.
 PA (LEXI-) LEXICON GENETICS INC.
 Query Match 12.1%; Score 56; DB 4; Length 877;
 Best Local Similarity 29.9%; Pred. No. 2.6e+03;
 RESULT 897
 ID AAE09852 standard; protein; 926 AA.
 DE Novel human protein (NHP) #18.
 PN WO200164718-A2.
 PD 07-SEP-2001.
 PA (LEXI-) LEXICON GENETICS INC.
 Query Match 12.1%; Score 56; DB 4; Length 926;
 Best Local Similarity 29.9%; Pred. No. 2.9e+03;
 RESULT 898
 ID ADJ50369 standard; protein; 960 AA.
 DE Oil-associated gene related protein #1869.
 PN US2004025202-A1.
 PD 05-FEB-2004.
 PA (LAUR/) LAURIE C C.
 PA (RAVA/) RAVANELLO M.
 PA (SAVA/) SAVAGE T.
 PA (LEDE/) LEDEAUX J R.
 PA (ROGE/) ROGERS J A.
 Query Match 12.1%; Score 56; DB 8; Length 960;
 Best Local Similarity 36.2%; Pred. No. 3e+03;
 RESULT 899
 ID AAE09854 standard; protein; 961 AA.
 DE Novel human protein (NHP) #20.
 PN WO200164718-A2.
 PD 07-SEP-2001.
 PA (LEXI-) LEXICON GENETICS INC.
 Query Match 12.1%; Score 56; DB 4; Length 961;
 Best Local Similarity 29.9%; Pred. No. 3e+03;
 RESULT 900
 ID AAB20015 standard; protein; 992 AA.
 DE Drosophila site 1 protease S1P homologue (dsip).
 PN WO200076308-A1.
 PD 21-DEC-2000.
 PA (EXEL-) EXELIXIS INC.
 Query Match 12.1%; Score 56; DB 4; Length 992;
 Best Local Similarity 29.2%; Pred. No. 3.1e+03;
 RESULT 901
 ID AAP80810 standard; protein; 1014 AA.
 DE Sequence of pol protein of HIV-2 ROD isolate CNM number I-532 in clone HIV-2.P.
 PN WO8805440-A.
 PD 28-JUL-1988.
 PA (INSP) INST PASTEUR.
 PA (ALIZ/) ALIZON M.

PA (CNRS) CENT NAT RECH SCI.
Query Match 12.1%; Score 56; DB 1; Length 1014;
Best Local Similarity 24.5%; Pred. No. 3.2e+03;
RESULT 902
ID AAR20599 standard; protein; 1036 AA.
DE ROD HIV-2 polymerase.
PN US5079342-A.
PD 07-JAN-1992.
PA (INSP) INST PASTEUR.
Query Match 12.1%; Score 56; DB 2; Length 1036;
Best Local Similarity 24.5%; Pred. No. 3.3e+03;
RESULT 903
ID AAY51978 standard; protein; 1036 AA.
DE HIV-2 ROD isolate polymerase DNA fragment.
PN US6054565-A.
PD 25-APR-2000.
PA (INSP) INST PASTEUR.
Query Match 12.1%; Score 56; DB 3; Length 1036;
Best Local Similarity 24.5%; Pred. No. 3.3e+03;
RESULT 904
ID ADA07961 standard; protein; 1036 AA.
DE HIV-2 polymerase.
PN US6544728-B1.
PD 08-APR-2003.
PA (INSP) INST PASTEUR.
Query Match 12.1%; Score 56; DB 6; Length 1036;
Best Local Similarity 24.5%; Pred. No. 3.3e+03;
RESULT 905
ID ADJ23699 standard; protein; 1036 AA.
DE HIV-2 ROD isolate polymerase protein.
PN US2003235835-A1.
PD 25-DEC-2003.
PA (INSP) INST PASTEUR.
Query Match 12.1%; Score 56; DB 8; Length 1042;
Best Local Similarity 24.5%; Pred. No. 3.4e+03;
RESULT 907
ID AAE09844 standard; protein; 1043 AA.
DE Novel human protein (NHP) #10.
PN WO200164718-A2.
PD 07-SEP-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 12.1%; Score 56; DB 4; Length 1043;
Best Local Similarity 29.9%; Pred. No. 3.4e+03;
RESULT 908
ID AAY13443 standard; protein; 1081 AA.
DE Amino acid sequence of hsl03-2.
PN WO9920754-A1.
PD 29-APR-1999.
PA (UNIW) UNIV WASHINGTON.
Query Match 12.1%; Score 56; DB 2; Length 1081;
Best Local Similarity 52.6%; Pred. No. 3.5e+03;
RESULT 909
ID ABG20256 standard; protein; 1086 AA.
DE Novel human diagnostic protein #20247.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.1%; Score 56; DB 4; Length 1086;
Best Local Similarity 32.8%; Pred. No. 3.6e+03;
RESULT 910
ID AAE09840 standard; protein; 1091 AA.
DE Novel human protein (NHP) #6.
PN WO200164718-A2.
PD 07-SEP-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 12.1%; Score 56; DB 4; Length 1091;
Best Local Similarity 29.9%; Pred. No. 3.6e+03;
RESULT 911
ID AAE09846 standard; protein; 1092 AA.
DE Novel human protein (NHP) #12.
PN WO200164718-A2.
PD 07-SEP-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 12.1%; Score 56; DB 4; Length 1092;
Best Local Similarity 29.9%; Pred. No. 3.6e+03;
RESULT 912
ID AAY13442 standard; protein; 1105 AA.
DE Amino acid sequence of hsl03-1.
PN WO9920754-A1.
PD 29-APR-1999.
PA (UNIW) UNIV WASHINGTON.
Query Match 12.1%; Score 56; DB 2; Length 1105;
Best Local Similarity 52.6%; Pred. No. 3.7e+03;
RESULT 913
ID ADJ49373 standard; protein; 1108 AA.
DE Oil-associated gene related protein #873.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEUX J R.
PA (ROGE/) ROGERS J A.
Query Match 12.1%; Score 56; DB 8; Length 1108;
Best Local Similarity 36.2%; Pred. No. 3.7e+03;
RESULT 914
ID ADJ49646 standard; protein; 1108 AA.
DE Oil-associated gene related protein #1146.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEUX J R.
PA (ROGE/) ROGERS J A.
Query Match 12.1%; Score 56; DB 8; Length 1108;
Best Local Similarity 36.2%; Pred. No. 3.7e+03;
RESULT 915
ID ADF16219 standard; protein; 1110 AA.
DE Human albumin therapeutic fusion protein SeqIDI306.
PN WO2003060071-A2.
PD 24-JUL-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (DELZ) DELTA BIOTECHNOLOGY LTD.
PA (PRIN-) PRINCIPIA PHARM CORP.
Query Match 12.1%; Score 56; DB 7; Length 1110;
Best Local Similarity 31.2%; Pred. No. 3.7e+03;
RESULT 916
ID AAE09842 standard; protein; 1126 AA.
DE Novel human protein (NHP) #8.
PN WO200164718-A2.
PD 07-SEP-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 12.1%; Score 56; DB 4; Length 1126;
Best Local Similarity 29.9%; Pred. No. 3.8e+03;
RESULT 917
ID AAE09848 standard; protein; 1127 AA.
DE Novel human protein (NHP) #14.
PN WO200164718-A2.
PD 07-SEP-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 12.1%; Score 56; DB 4; Length 1127;
Best Local Similarity 29.9%; Pred. No. 3.8e+03;
RESULT 918
ID ABR53342 standard; protein; 1138 AA.
DE Protein sequence #SEQ ID 1549.
PN EPI258494-A1.
PD 20-NOV-2002.

PA (CELL-) CELLZOME AG.
Query Match 12.1%; Score 56; DB 6; Length 1138;
Best Local Similarity 26.7%; Pred. No. 3.8e+03;
RESULT 919
ID ADK63426 standard; protein; 1138 AA.
DE Disease treating protein complex-derived protein #940.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 12.1%; Score 56; DB 7; Length 1138;
Best Local Similarity 26.7%; Pred. No. 3.8e+03;
RESULT 920
ID ABP73963 standard; protein; 1363 AA.
DE Candida albicans essential protein SEQ ID NO 7800.
PN WO200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.1%; Score 56; DB 5; Length 1363;
Best Local Similarity 20.9%; Pred. No. 4.9e+03;
RESULT 921
ID AAR92768 standard; protein; 1394 AA.
DE Adhesion and penetration protein.
PN WO9605858-A1.
PD 29-FEB-1996.
PA (UNIW) UNIV WASHINGTON.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 12.1%; Score 56; DB 2; Length 1394;
Best Local Similarity 31.5%; Pred. No. 5.1e+03;
RESULT 922
ID ADA09343 standard; protein; 1394 AA.
DE Haemophilus adherence and penetration protein (HAP).
PN US2003073166-A1.
PD 17-APR-2003.
PA (GEME/) GEME J W S.
Query Match 12.1%; Score 56; DB 6; Length 1394;
Best Local Similarity 31.5%; Pred. No. 5.1e+03;
RESULT 923
ID AAY38825 standard; protein; 1468 AA.
DE Neisseria gonorrhoeae antigenic protein encoded by ORF1.
PN WO9924578-A2.
PD 20-MAY-1999.
PA (CHIR-) CHIRON SPA.
Query Match 12.1%; Score 56; DB 2; Length 1468;
Best Local Similarity 30.4%; Pred. No. 5.4e+03;
RESULT 924
ID ABP77279 standard; protein; 1468 AA.
DE N. gonorrhoeae amino acid sequence SEQ ID 1088.
PN WO200273243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Query Match 12.1%; Score 56; DB 6; Length 1468;
Best Local Similarity 30.4%; Pred. No. 5.4e+03;
RESULT 925
ID ABU37103 standard; protein; 1468 AA.
DE Protein encoded by Prokaryotic essential gene #22630.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.1%; Score 56; DB 6; Length 1468;
Best Local Similarity 30.4%; Pred. No. 5.4e+03;
RESULT 926
ID AAW29322 standard; protein; 1829 AA.
DE DNA polymerase with 3'-5' exonuclease activity.
PN DE19611759-A1.
PD 02-OCT-1997.
PA (BOEF) BOEHRINGER MANNHEIM GMBH.
Query Match 12.1%; Score 56; DB 2; Length 1829;
Best Local Similarity 22.8%; Pred. No. 7.4e+03;
RESULT 927
ID ADN59952 standard; protein; 1829 AA.
DE Thermococcus strain TY DNA polymerase protein SEQ ID NO:13.
PN WO2004039947-A2.
PD 13-MAY-2004.

PA (STRA-) STRATAGENE.
Query Match 12.1%; Score 56; DB 8; Length 1829;
Best Local Similarity 22.8%; Pred. No. 7.4e+03;
RESULT 928
ID BCU58318 standard; protein; 2633 AA.
DE BCU0205B protein #SEQ ID 82.
PN WO2003029421-A2.
PD 10-APR-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 12.1%; Score 56; DB 6; Length 2633;
Best Local Similarity 31.5%; Pred. No. 1.2e+04;
RESULT 929
ID ADH71218 standard; protein; 2662 AA.
DE Human protein of the invention NOV7a SEQ ID NO:114.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.1%; Score 56; DB 8; Length 2662;
Best Local Similarity 31.5%; Pred. No. 1.3e+04;
RESULT 930
ID AAU08681 standard; protein; 2724 AA.
DE Human FCTR3f polypeptide sequence.
PN WO200166747-A2.
PD 13-SEP-2001.
PA (CURA-) CURAGEN CORP.
Query Match 12.1%; Score 56; DB 4; Length 2724;
Best Local Similarity 31.5%; Pred. No. 1.3e+04;
RESULT 931
ID ADB32029 standard; protein; 2724 AA.
DE Human FCTR3f polypeptide.
PN US2003087816-A1.
PD 08-MAY-2003.
PA (VERM/) VERMET C.
PA (FERN/) FERNANDES E.
PA (SHIM/) SHIMKETS R.
PA (HERR/) HERRMANN J.
PA (MAJU/) MAJUMDER K.
PA (MACD/) MACDOUGALL J.
PA (MISH/) MISHRA V.
PA (MEZE/) MEZES P S.
PA (RAST/) RASTELLI L.
Query Match 12.1%; Score 56; DB 7; Length 2724;
Best Local Similarity 31.5%; Pred. No. 1.3e+04;
RESULT 932
ID ADH71252 standard; protein; 2724 AA.
DE Human protein of the invention NOV7r SEQ ID NO:148.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.1%; Score 56; DB 8; Length 2724;
Best Local Similarity 31.5%; Pred. No. 1.3e+04;
RESULT 933
ID AAU08680 standard; protein; 2733 AA.
DE Human FCTR3b polypeptide sequence.
PN WO200166747-A2.
PD 13-SEP-2001.
PA (CURA-) CURAGEN CORP.
Query Match 12.1%; Score 56; DB 4; Length 2733;
Best Local Similarity 31.5%; Pred. No. 1.3e+04;
RESULT 934
ID ADB32024 standard; protein; 2733 AA.
DE Human FCTR3b polypeptide.
PN US2003087816-A1.
PD 08-MAY-2003.
PA (VERM/) VERMET C.
PA (FERN/) FERNANDES E.
PA (SHIM/) SHIMKETS R.
PA (HERR/) HERRMANN J.
PA (MAJU/) MAJUMDER K.
PA (MACD/) MACDOUGALL J.
PA (MISH/) MISHRA V.
PA (MEZE/) MEZES P S.
PA (RAST/) RASTELLI L.

Query Match 12.1%; Score 56; DB 7; Length 2733;
Best Local Similarity 31.5%; Pred. No. 1.3e+04;
RESULT 935
ID ADH71250 standard; protein; 2733 AA.
DE Human protein of the invention NOV7q SEQ ID NO:146.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.1%; Score 56; DB 8; Length 2733;
Best Local Similarity 31.5%; Pred. No. 1.3e+04;
RESULT 936
ID ADH71254 standard; protein; 2733 AA.
DE Human protein of the invention NOV7s SEQ ID NO:150.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.1%; Score 56; DB 8; Length 2733;
Best Local Similarity 31.5%; Pred. No. 1.3e+04;
RESULT 937
ID ADH71240 standard; protein; 2733 AA.
DE Human protein of the invention NOV7l SEQ ID NO:136.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.1%; Score 56; DB 8; Length 2733;
Best Local Similarity 31.5%; Pred. No. 1.3e+04;
RESULT 938
ID ADH71246 standard; protein; 2733 AA.
DE Human protein of the invention NOV7o SEQ ID NO:142.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.1%; Score 56; DB 8; Length 2733;
Best Local Similarity 31.5%; Pred. No. 1.3e+04;
RESULT 939
ID ADH71258 standard; protein; 2733 AA.
DE Human protein of the invention NOV7u SEQ ID NO:154.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.1%; Score 56; DB 8; Length 2733;
Best Local Similarity 31.5%; Pred. No. 1.3e+04;
RESULT 940
ID ADI16951 standard; protein; 2764 AA.
DE Murine NOVX protein homologue SeqID 488.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 12.1%; Score 56; DB 5; Length 2764;
Best Local Similarity 31.5%; Pred. No. 1.3e+04;
RESULT 941
ID ADJ76262 standard; protein; 2764 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1514.
PN EPI394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 12.1%; Score 56; DB 8; Length 2764;
Best Local Similarity 31.5%; Pred. No. 1.3e+04;
RESULT 942
ID ADI16952 standard; protein; 2765 AA.
DE Rat NOVX protein homologue SeqID 489.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 12.1%; Score 56; DB 5; Length 2765;
Best Local Similarity 31.5%; Pred. No. 1.3e+04;
RESULT 943
ID ADH71220 standard; protein; 2765 AA.
DE Human protein of the invention NOV7b SEQ ID NO:116.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.1%; Score 56; DB 8; Length 2765;
Best Local Similarity 31.5%; Pred. No. 1.3e+04;
RESULT 944
ID AAP93285 standard; protein; 3080 AA.
DE Sequence of clone HIV-2 SBL/ISY.
PN UGN7331212-N.
PD 29-AUG-1989.
PA (USSH) US DEPT HEALTH & HUMAN SERVICE.
PA (USDC) US SEC OF COMMERCE.
PA (USDC) US SEC OF COMMERCE.
Query Match 12.1%; Score 56; DB 1; Length 3080;
Best Local Similarity 33.3%; Pred. No. 1.5e+04;
RESULT 945
ID ADC71249 standard; protein; 93 AA.
DE Human colon specific protein sequence DEX0235_77 (SeqID 77).
PN WO2003020934-A1.
PD 13-MAR-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 12.0%; Score 55.5; DB 7; Length 93;
Best Local Similarity 30.3%; Pred. No. 1.3e+02;
RESULT 946
ID AAO17070 standard; protein; 104 AA.
DE Bovine thymus nucleolin derived antibiotic peptide.
PN WO200194386-A2.
PD 13-DEC-2001.
PA (IPFP-) IPF PHARM GMBH.
Query Match 12.0%; Score 55.5; DB 5; Length 104;
Best Local Similarity 41.0%; Pred. No. 1.5e+02;
RESULT 947
ID AAM82492 standard; protein; 120 AA.
DE Human immune/haematopoietic antigen SEQ ID NO:10085.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.0%; Score 55.5; DB 4; Length 120;
Best Local Similarity 36.2%; Pred. No. 1.9e+02;
RESULT 948
ID AAY00094 standard; protein; 122 AA.
DE Enterococcus faecalis protein EF046.
PN WO9850554-A2.
PD 12-NOV-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.0%; Score 55.5; DB 2; Length 122;
Best Local Similarity 32.9%; Pred. No. 1.9e+02;
RESULT 949
ID ABP43313 standard; protein; 122 AA.
DE E faecalis EF046 protein.
PN US2002045737-A1.
PD 18-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.0%; Score 55.5; DB 5; Length 122;
Best Local Similarity 32.9%; Pred. No. 1.9e+02;
RESULT 950
ID ABU88341 standard; protein; 122 AA.
DE E. faecalis novel protein #85.
PN US2003017495-A1.
PD 23-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.0%; Score 55.5; DB 6; Length 122;
Best Local Similarity 32.9%; Pred. No. 1.9e+02;
RESULT 951
ID ABU13592 standard; protein; 122 AA.
DE Enterococcus faecalis EF040 polypeptide #85.
PN US6448043-B1.
PD 10-SEP-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.0%; Score 55.5; DB 6; Length 122;
Best Local Similarity 32.9%; Pred. No. 1.9e+02;
RESULT 952
ID ABG06040 standard; protein; 126 AA.
DE Novel human diagnostic protein #6031.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.

Query Match 12.0%; Score 55.5; DB 4; Length 126;
Best Local Similarity 27.4%; Pred. No. 2e+02;
RESULT 953
ID AAR62755 standard; protein; 148 AA.
DE SefD sequence.
PN WO9425598-A2.
PD 10-NOV-1994.
PA (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
PA (KING/) KING J.
Query Match 12.0%; Score 55.5; DB 2; Length 148;
Best Local Similarity 28.2%; Pred. No. 2.5e+02;
RESULT 954
ID AAW23574 standard; protein; 148 AA.
DE Salmonella enteritidis sefd.
PN US5635617-A.
PD 03-JUN-1997.
PA (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
Query Match 12.0%; Score 55.5; DB 2; Length 148;
Best Local Similarity 28.2%; Pred. No. 2.5e+02;
RESULT 955
ID ABB05659 standard; protein; 169 AA.
DE Zephyranthes candida agglutinin (z-lectin) protein SEQ ID NO:4.
PN CN1323887-A.
PD 28-NOV-2001.
PA (SHAN-) SHANGHAI FUDAN DIEN BIOLOGICAL TECHN CO.
Query Match 12.0%; Score 55.5; DB 5; Length 169;
Best Local Similarity 27.3%; Pred. No. 3e+02;
RESULT 956
ID AAU51918 standard; protein; 170 AA.
DE Propionibacterium acnes immunogenic protein #12814.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 12.0%; Score 55.5; DB 4; Length 170;
Best Local Similarity 33.3%; Pred. No. 3e+02;
RESULT 957
ID ABM48437 standard; protein; 170 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #13113.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 12.0%; Score 55.5; DB 6; Length 170;
Best Local Similarity 33.3%; Pred. No. 3e+02;
RESULT 958
ID ABP30107 standard; protein; 174 AA.
DE Streptococcus polypeptide SEQ ID NO 9390.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 12.0%; Score 55.5; DB 5; Length 174;
Best Local Similarity 24.1%; Pred. No. 3.1e+02;
RESULT 959
ID ADH12913 standard; protein; 186 AA.
DE Francisella tularensis immunogenic protein 94, SEQ ID NO:94.
PN WO2004003009-A2.
PD 08-JAN-2004.
PA (MINA) UK SEC FOR DEFENCE.
Query Match 12.0%; Score 55.5; DB 8; Length 186;
Best Local Similarity 28.1%; Pred. No. 3.5e+02;
RESULT 960
ID ADJ69338 standard; protein; 216 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1144.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 12.0%; Score 55.5; DB 7; Length 216;
Best Local Similarity 28.4%; Pred. No. 4.3e+02;
RESULT 961
ID AAW80748 standard; protein; 217 AA.
DE Human mitochondrial chaperone protein (Hmt-GrpE).
PN WO9842837-A1.

PD 01-OCT-1998.
PA (INCY-) INCYTE PHARM INC.
Query Match 12.0%; Score 55.5; DB 2; Length 217;
Best Local Similarity 28.4%; Pred. No. 4.3e+02;
RESULT 962
ID AAU27779 standard; protein; 217 AA.
DE Human full-length polypeptide sequence #104.
PN WO200164834-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.0%; Score 55.5; DB 4; Length 217;
Best Local Similarity 28.4%; Pred. No. 4.3e+02;
RESULT 963
ID AAG64577 standard; protein; 217 AA.
DE Human GrpE protein.
PN CN1297921-A.
PD 06-JUN-2001.
PA (SHAN-) SHANGHAI BORONG GENE TECHNOLOGY CO LTD.
Query Match 12.0%; Score 55.5; DB 4; Length 217;
Best Local Similarity 28.4%; Pred. No. 4.3e+02;
RESULT 964
ID ABR64187 standard; protein; 217 AA.
DE Angiogenesis protein BNO92.
PN WO2003027285-A1.
PD 03-APR-2003.
PA (BION-) BIONOMICS LTD.
Query Match 12.0%; Score 55.5; DB 6; Length 217;
Best Local Similarity 28.4%; Pred. No. 4.3e+02;
RESULT 965
ID ADJ70957 standard; protein; 217 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID2763.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 12.0%; Score 55.5; DB 7; Length 217;
Best Local Similarity 28.4%; Pred. No. 4.3e+02;
RESULT 966
ID ABB69807 standard; protein; 220 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 36213.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.0%; Score 55.5; DB 4; Length 220;
Best Local Similarity 28.8%; Pred. No. 4.4e+02;
RESULT 967
ID AAY85938 standard; protein; 246 AA.
DE S. pneumoniae derived protein #147.
PN WO9806734-A1.
PD 19-FEB-1998.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 12.0%; Score 55.5; DB 2; Length 246;
Best Local Similarity 30.1%; Pred. No. 5.1e+02;
RESULT 968
ID ADM74711 standard; protein; 247 AA.
DE Fusarium oxysporum trypsinogen-like mutant protein - V192*.
PN WO2004029202-A2.
PD 08-APR-2004.
PA (NOVO) NOVOZYMES BIOTECH INC.
Query Match 12.0%; Score 55.5; DB 8; Length 247;
Best Local Similarity 21.0%; Pred. No. 5.1e+02;
RESULT 969
ID AAB10283 standard; protein; 255 AA.
DE Human fetal kidney protein fragment AA36_1i.
PN WO200037630-A1.
PD 29-JUN-2000.
PA (GEWY) GENETICS INST INC.
Query Match 12.0%; Score 55.5; DB 3; Length 255;
Best Local Similarity 28.3%; Pred. No. 5.4e+02;
RESULT 970
ID AAU19292 standard; protein; 321 AA.
DE Human G protein-coupled receptor nGPCR-74.
PN WO200166750-A2.

PD 13-SEP-2001.
PA (PHAA) PHARMACIA & UPJOHN CO.
Query Match 12.0%; Score 55.5; DB 4; Length 321;
Best Local Similarity 26.3%; Pred. No. 7.4e+02;
RESULT 971
ID AAG65582 standard; protein; 321 AA.
DE Human RTA-like G protein-coupled receptor polypeptide.
PN WO200170814-A2.
PD 27-SEP-2001.
PA (FARB) BAYER AG.
Query Match 12.0%; Score 55.5; DB 4; Length 321;
Best Local Similarity 26.3%; Pred. No. 7.4e+02;
RESULT 972
ID AAS06768 standard; protein; 321 AA.
DE Human G-protein coupled receptor-18 (GPRC-18) protein.
PN WO200157085-A2.
PD 09-AUG-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 12.0%; Score 55.5; DB 4; Length 321;
Best Local Similarity 26.3%; Pred. No. 7.4e+02;
RESULT 973
ID AAG64124 standard; protein; 321 AA.
DE Human G protein-coupled receptor GPRV51.
PN WO200148188-A1.
PD 05-JUL-2001.
PA (HELI-) HELIX RES INST.
Query Match 12.0%; Score 55.5; DB 4; Length 321;
Best Local Similarity 26.3%; Pred. No. 7.4e+02;
RESULT 974
ID AAU04366 standard; protein; 321 AA.
DE Human G-protein coupled receptor, hRUP12.
PN WO200136471-A2.
PD 25-MAY-2001.
PA (AREN-) ARENA PHARM INC.
Query Match 12.0%; Score 55.5; DB 4; Length 321;
Best Local Similarity 26.3%; Pred. No. 7.4e+02;
RESULT 975
ID ABB04658 standard; protein; 321 AA.
DE Human G protein-coupled receptor TGR7 SEQ ID NO:1.
PN WO200183748-A1.
PD 08-NOV-2001.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 12.0%; Score 55.5; DB 5; Length 321;
Best Local Similarity 26.3%; Pred. No. 7.4e+02;
RESULT 976
ID AAE17075 standard; protein; 321 AA.
DE Human G-protein coupled receptor (GPCRx7) protein.
PN WO200198330-A2.
PD 27-DEC-2001.
PA (EURO-) EUROSREEN SA.
Query Match 12.0%; Score 55.5; DB 5; Length 321;
Best Local Similarity 26.3%; Pred. No. 7.4e+02;
RESULT 977
ID ABB08770 standard; protein; 321 AA.
DE Human G-protein coupled receptor SEQ ID NO 2.
PN EP1178053-A2.
PD 06-FEB-2002.
PA (SWIT-) SWITCH BIOTECH AG.
Query Match 12.0%; Score 55.5; DB 5; Length 321;
Best Local Similarity 26.3%; Pred. No. 7.4e+02;
RESULT 978
ID ABP95616 standard; protein; 321 AA.
DE Human GPCR polypeptide SEQ ID NO 42.
PN WO200216548-A2.
PD 28-FEB-2002.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 12.0%; Score 55.5; DB 5; Length 321;
Best Local Similarity 26.3%; Pred. No. 7.4e+02;
RESULT 979
ID ABP96694 standard; protein; 321 AA.
DE Human G protein-coupled receptor DRG6 protein SEQ ID NO:8.
PN WO2003023010-A2.
PD 20-MAR-2003.

PA (IRMI-) IRM LLC.
Query Match 12.0%; Score 55.5; DB 6; Length 321;
Best Local Similarity 26.3%; Pred. No. 7.4e+02;
RESULT 980
ID ABP71374 standard; protein; 321 AA.
DE Human TGR2 protein.
PN WO2003004678-A2.
PD 16-JAN-2003.
PA (TULIA-) TULARIK INC.
Query Match 12.0%; Score 55.5; DB 6; Length 321;
Best Local Similarity 26.3%; Pred. No. 7.4e+02;
RESULT 981
ID ABE62311 standard; protein; 321 AA.
DE Human G-protein coupled receptor HGRBMY31 splice variant.
PN WO2003046147-A2.
PD 05-JUN-2003.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 12.0%; Score 55.5; DB 6; Length 321;
Best Local Similarity 26.3%; Pred. No. 7.4e+02;
RESULT 982
ID ADC39134 standard; protein; 321 AA.
DE Novel human NOVX polypeptide SEQ ID NO: 76.
PN WO2003010327-A2.
PD 06-FEB-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.0%; Score 55.5; DB 7; Length 321;
Best Local Similarity 26.3%; Pred. No. 7.4e+02;
RESULT 983
ID ABW08005 standard; protein; 321 AA.
DE Human GPCRx7 protein.
PN US2003108986-A1.
PD 12-JUN-2003.
PA (EURO-) EUROSREEN SA.
Query Match 12.0%; Score 55.5; DB 7; Length 321;
Best Local Similarity 26.3%; Pred. No. 7.4e+02;
RESULT 984
ID ADD29438 standard; protein; 321 AA.
DE Human G-protein coupled receptor amino acid sequence.
PN WO2003082320-A1.
PD 09-OCT-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 12.0%; Score 55.5; DB 7; Length 321;
Best Local Similarity 26.3%; Pred. No. 7.4e+02;
RESULT 985
ID ADL96456 standard; protein; 321 AA.
DE Human G protein-coupled receptor (GPCR) polypeptide #5.
PN US2003166148-A1.
PD 04-SEP-2003.
PA (CHEN/) CHEN R.
PA (DANG/) DANG H T.
PA (LOWI/) LOWITZ K P.
Query Match 12.0%; Score 55.5; DB 7; Length 321;
Best Local Similarity 26.3%; Pred. No. 7.4e+02;
RESULT 986
ID ADH08539 standard; protein; 321 AA.
DE hMrgD.
PN WO2004003133-A1.
PD 08-JAN-2004.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
Query Match 12.0%; Score 55.5; DB 8; Length 321;
Best Local Similarity 26.3%; Pred. No. 7.4e+02;
RESULT 987
ID ADO29546 standard; protein; 321 AA.
DE Human GPCR MRGD, SEQ ID NO:648.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 12.0%; Score 55.5; DB 8; Length 321;
Best Local Similarity 26.3%; Pred. No. 7.4e+02;
RESULT 988
ID ADC86439 standard; protein; 347 AA.
DE Human GPCR protein SEQ ID NO:892.
PN EP1270724-A2.

PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 12.0%; Score 55.5; DB 7; Length 347;
Best Local Similarity 26.3%; Pred. No. 8.3e+02;
RESULT 989
ID ADC33236 standard; protein; 354 AA.
DE Human novel contig-encoded polypeptide sequence, SEQ ID NO:3318.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 12.0%; Score 55.5; DB 7; Length 354;
Best Local Similarity 26.5%; Pred. No. 8.5e+02;
RESULT 990
ID ABP40788 standard; protein; 358 AA.
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5633.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.0%; Score 55.5; DB 5; Length 358;
Best Local Similarity 32.1%; Pred. No. 8.7e+02;
RESULT 991
ID ABU25507 standard; protein; 359 AA.
DE Protein encoded by Prokaryotic essential gene #11034.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.0%; Score 55.5; DB 6; Length 359;
Best Local Similarity 23.5%; Pred. No. 8.7e+02;
RESULT 992
ID AAM411801 standard; protein; 367 AA.
DE Human polypeptide SEQ ID NO 6732.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.0%; Score 55.5; DB 4; Length 367;
Best Local Similarity 32.0%; Pred. No. 9e+02;
RESULT 993
ID AAG66006 standard; protein; 369 AA.
DE F. necrophorum truncated leukotoxin protein (BSBSE).
PN WO200108086-A2.
PD 01-NOV-2001.
PA (UNIV) UNIV KANSAS STATE RES FOUND.
Query Match 12.0%; Score 55.5; DB 5; Length 369;
Best Local Similarity 33.3%; Pred. No. 9e+02;
RESULT 994
ID AAW73513 standard; protein; 388 AA.
DE Rabbit TGFbetaRII:Fc protein.
PN WO9848024-A1.
PD 29-OCT-1998.
PA (BIOJ) BIOGEN INC.
Query Match 12.0%; Score 55.5; DB 2; Length 388;
Best Local Similarity 28.1%; Pred. No. 9.7e+02;
RESULT 995
ID AAY54063 standard; protein; 388 AA.
DE Amino acid sequence of TGF-beta type II receptor variant/IgG1 fusion.
PN WO965948-A1.
PD 23-DEC-1999.
PA (BIOJ) BIOGEN INC.
Query Match 12.0%; Score 55.5; DB 3; Length 388;
Best Local Similarity 28.1%; Pred. No. 9.7e+02;
RESULT 996
ID AAB70114 standard; protein; 391 AA.
DE Murine 3-OST-3B.
PN WO200113910-A2.
PD 01-MAR-2001.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
PA (NOUN) UNIV NORTHWESTERN.
Query Match 12.0%; Score 55.5; DB 4; Length 391;
Best Local Similarity 27.5%; Pred. No. 9.8e+02;
RESULT 997
ID ADC31635 standard; protein; 394 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1717.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 12.0%; Score 55.5; DB 7; Length 394;
Best Local Similarity 26.5%; Pred. No. 9.9e+02;
RESULT 998
ID ABM68272 standard; protein; 398 AA.
DE Photorhabdus luminescens protein sequence #1369.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 12.0%; Score 55.5; DB 6; Length 398;
Best Local Similarity 29.2%; Pred. No. 1e+03;
RESULT 999
ID ARG00935 standard; protein; 400 AA.
DE Novel human diagnostic protein #926.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.0%; Score 55.5; DB 4; Length 400;
Best Local Similarity 20.6%; Pred. No. 1e+03;
RESULT 1000
ID ABO00906 standard; protein; 400 AA.
DE Polypeptide encoded by novel human contig #157.
PN WO2003023013-A2.
PD 20-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 12.0%; Score 55.5; DB 6; Length 400;
Best Local Similarity 20.6%; Pred. No. 1e+03;
RESULT 1001
ID ABO00679 standard; protein; 400 AA.
DE Novel human polypeptide #266.
PN WO2003023013-A2.
PD 20-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 12.0%; Score 55.5; DB 6; Length 400;
Best Local Similarity 20.6%; Pred. No. 1e+03;
RESULT 1002
ID ABB67174 standard; protein; 436 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 28314.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.0%; Score 55.5; DB 4; Length 436;
Best Local Similarity 26.6%; Pred. No. 1.1e+03;
RESULT 1003
ID ABU39822 standard; protein; 436 AA.
DE Protein encoded by Prokaryotic essential gene #25349.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.0%; Score 55.5; DB 6; Length 436;
Best Local Similarity 26.9%; Pred. No. 1.1e+03;
RESULT 1004
ID ABP41244 standard; protein; 440 AA.
DE Human ovarian antigen HSUA20, SEQ ID NO:2376.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.0%; Score 55.5; DB 5; Length 440;
Best Local Similarity 20.4%; Pred. No. 1.2e+03;
RESULT 1005
ID AAM93699 standard; protein; 441 AA.
DE Human polypeptide, SEQ ID NO: 3620.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 12.0%; Score 55.5; DB 4; Length 441;
Best Local Similarity 26.5%; Pred. No. 1.2e+03;
RESULT 1006
ID ADL31587 standard; protein; 441 AA.
DE Human protein encoded by a full length cDNA clone SeqID 3620.

PN EPI396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 12.0%; Score 55.5; DB 8; Length 441;
Best Local Similarity 26.5%; Pred. No. 1.2e+03;
RESULT 1007
ID ADK40930 standard; protein; 444 AA.
DE Novel human kinase protein #37.
PN WO2003057841-A2.
PD 17-JUL-2003.
PA (GRIG/) GRIGORIEV I V.
PA (SUDA/) SUDARSANAM S.
Query Match 12.0%; Score 55.5; DB 7; Length 444;
Best Local Similarity 26.5%; Pred. No. 1.2e+03;
RESULT 1008
ID AB028233 standard; protein; 450 AA.
DE Protein encoded by Prokaryotic essential gene #13760.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.0%; Score 55.5; DB 6; Length 450;
Best Local Similarity 32.1%; Pred. No. 1.2e+03;
RESULT 1009
ID ABG18986 standard; protein; 462 AA.
DE Novel human diagnostic protein #18877.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.0%; Score 55.5; DB 4; Length 462;
Best Local Similarity 32.3%; Pred. No. 1.2e+03;
RESULT 1010
ID AA27177 standard; protein; 467 AA.
DE Human mutant S182 gene, PSI, product related to Alzheimer's disease.
PN WO9708319-A1.
PD 06-MAR-1997.
PA (GHHO) GEN HOSPITAL CORP.
Query Match 12.0%; Score 55.5; DB 2; Length 467;
Best Local Similarity 20.0%; Pred. No. 1.3e+03;
RESULT 1011
ID AA27176 standard; protein; 467 AA.
DE Human S182 gene, PSI locus, product related to Alzheimer's disease.
PN WO9708319-A1.
PD 06-MAR-1997.
PA (GHHO) GEN HOSPITAL CORP.
Query Match 12.0%; Score 55.5; DB 2; Length 467;
Best Local Similarity 20.0%; Pred. No. 1.3e+03;
RESULT 1012
ID AFU62335 standard; protein; 468 AA.
DE SFPA L42R/SPEB C47S mutant fusion protein.
PN US2003036644-A1.
PD 20-FEB-2003.
PA (URI/) URICH R G.
Query Match 12.0%; Score 55.5; DB 7; Length 468;
Best Local Similarity 30.1%; Pred. No. 1.3e+03;
RESULT 1013
ID AAB37684 standard; protein; 468 AA.
DE Streptococcus pyogenes SpeA-SpeB fusion protein.
PN WC2003056015-A1.
PD 10-JUL-2003.
PA (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
Query Match 12.0%; Score 55.5; DB 7; Length 468;
Best Local Similarity 30.1%; Pred. No. 1.3e+03;
RESULT 1014
ID AAB37691 standard; protein; 468 AA.
DE S. pyogenes mature mutant SpeA-mature mutant SpeB fusion protein.
PN WC2003056015-A1.
PD 10-JUL-2003.
PA (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
Query Match 12.0%; Score 55.5; DB 7; Length 468;
Best Local Similarity 30.1%; Pred. No. 1.3e+03;
RESULT 1015
ID ADD69271 standard; protein; 491 AA.
DE Human fibrinogen beta protein 1 - SEQ ID 7.

PN WO2003048185-A2.
PD 12-JUN-2003.
PA (GENV-) GENVEC INC.
Query Match 12.0%; Score 55.5; DB 7; Length 491;
Best Local Similarity 30.5%; Pred. No. 1.3e+03;
RESULT 1016
ID ADD69272 standard; protein; 491 AA.
DE Human fibrinogen beta protein 2 - SEQ ID 8.
PN WO2003048185-A2.
PD 12-JUN-2003.
PA (GENV-) GENVEC INC.
Query Match 12.0%; Score 55.5; DB 7; Length 491;
Best Local Similarity 30.5%; Pred. No. 1.3e+03;
RESULT 1017
ID AAB42081 standard; protein; 504 AA.
DE Human ORFX ORF1845 polypeptide sequence SEQ ID NO:3690.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 12.0%; Score 55.5; DB 3; Length 504;
Best Local Similarity 34.8%; Pred. No. 1.4e+03;
RESULT 1018
ID ADC96367 standard; protein; 506 AA.
DE E. faecium protein sequence SEQ ID 5994.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.0%; Score 55.5; DB 7; Length 506;
Best Local Similarity 30.2%; Pred. No. 1.4e+03;
RESULT 1019
ID ABB64821 standard; protein; 510 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 21255.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.0%; Score 55.5; DB 4; Length 510;
Best Local Similarity 32.1%; Pred. No. 1.4e+03;
RESULT 1020
ID ABG18314 standard; protein; 526 AA.
DE Novel human diagnostic protein #18305.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.0%; Score 55.5; DB 4; Length 526;
Best Local Similarity 28.8%; Pred. No. 1.5e+03;
RESULT 1021
ID ABG66690 standard; protein; 526 AA.
DE Human novel polypeptide #25.
PN WO200244340-A2.
PD 06-JUN-2002.
PA (HYSE-) HYSEQ INC.
Query Match 12.0%; Score 55.5; DB 5; Length 526;
Best Local Similarity 36.2%; Pred. No. 1.5e+03;
RESULT 1022
ID ADO57303 standard; protein; 526 AA.
DE Kidney development associated protein segid 70.
PN US2004068763-A1.
PD 08-APR-2004.
PA (HOPK/) HOPKINS N.
PA (GOLL/) GOLLING G.
PA (AMST/) AMSTERDAM A.
PA (SUNZ/) SUN Z.
Query Match 12.0%; Score 55.5; DB 8; Length 526;
Best Local Similarity 28.4%; Pred. No. 1.5e+03;
RESULT 1023
ID AB073763 standard; protein; 531 AA.
DE Pseudomonas aeruginosa polypeptide #5938.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.0%; Score 55.5; DB 7; Length 531;
Best Local Similarity 25.9%; Pred. No. 1.5e+03;
RESULT 1024

RESULT 1033
ID AEG66689 standard; protein; 588 AA.
DE Human novel polypeptide #24.
PN WO200244340-A2.
PD 06-JUN-2002.
PA (HYSE-) HYSEQ INC.
Query Match 12.0%; Score 55.5; DB 5; Length 588;
Best Local Similarity 36.2%; Pred. No. 1.7e+03;
RESULT 1025
ID AAM52618 standard; protein; 616 AA.
DE Human replication protein A p70 subunit (RPA70) T351A variant.
PN US6309882-B1.
PD 30-OCT-2001.
PA (ISIS-) ISIS PHARM INC.
PA (VARI-) VARIAGENICS INC.
Query Match 12.0%; Score 55.5; DB 5; Length 616;
Best Local Similarity 20.4%; Pred. No. 1.9e+03;
RESULT 1026
ID AAM52617 standard; protein; 616 AA.
DE Human replication protein A p70 subunit (RPA70).
PN US6309882-B1.
PD 30-OCT-2001.
PA (ISIS-) ISIS PHARM INC.
PA (VARI-) VARIAGENICS INC.
Query Match 12.0%; Score 55.5; DB 5; Length 616;
Best Local Similarity 20.4%; Pred. No. 1.9e+03;
RESULT 1027
ID AAO30065 standard; protein; 616 AA.
DE Human replication protein A (RPA) #1.
PN WO2003044214-A2.
PD 30-MAY-2003.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
Query Match 12.0%; Score 55.5; DB 6; Length 616;
Best Local Similarity 20.4%; Pred. No. 1.9e+03;
RESULT 1028
ID ABB57783 standard; protein; 657 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 141.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.0%; Score 55.5; DB 4; Length 657;
Best Local Similarity 28.8%; Pred. No. 2e+03;
RESULT 1029
ID AAE01020 standard; protein; 689 AA.
DE Human pif-1 type helicase protein.
PN WO200130986-A2.
PD 03-MAY-2001.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 12.0%; Score 55.5; DB 4; Length 689;
Best Local Similarity 36.2%; Pred. No. 2.2e+03;
RESULT 1030
ID AAG82482 standard; protein; 720 AA.
DE S. epidermidis open reading frame protein sequence SEQ ID NO:2058.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 12.0%; Score 55.5; DB 4; Length 720;
Best Local Similarity 25.0%; Pred. No. 2.3e+03;
RESULT 1031
ID AAY72914 standard; protein; 725 AA.
DE E. coli ironNec extracytoplasmic protein fragment.
PN WO200121636-A1.
PD 29-MAR-2001.
PA (UYNV) UNIV NEW YORK STATE RES FOUND.
Query Match 12.0%; Score 55.5; DB 4; Length 725;
Best Local Similarity 29.5%; Pred. No. 2.3e+03;
RESULT 1032
ID ABP40123 standard; protein; 728 AA.
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4968.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.0%; Score 55.5; DB 5; Length 728;
Best Local Similarity 25.0%; Pred. No. 2.3e+03;

RESULT 1033
ID ABU43020 standard; protein; 728 AA.
DE Protein encoded by Prokaryotic essential gene #28547.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.0%; Score 55.5; DB 6; Length 728;
Best Local Similarity 25.0%; Pred. No. 2.3e+03;
RESULT 1034
ID ABU11737 standard; protein; 809 AA.
DE Human MDTT polypeptide SEQ ID 684.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 12.0%; Score 55.5; DB 6; Length 809;
Best Local Similarity 31.6%; Pred. No. 2.7e+03;
RESULT 1035
ID AAR22275 standard; protein; 839 AA.
DE Bovine liver GPI-PLD.
PN EP477739-A.
PD 01-APR-1992.
PA (HOFF) HOFFMANN-LA ROCHE AG.
Query Match 12.0%; Score 55.5; DB 2; Length 839;
Best Local Similarity 23.3%; Pred. No. 2.9e+03;
RESULT 1036
ID ABB63795 standard; protein; 865 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 18177.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.0%; Score 55.5; DB 4; Length 865;
Best Local Similarity 31.2%; Pred. No. 3e+03;
RESULT 1037
ID ADD18910 standard; protein; 892 AA.
DE Human disease related protein SeqID399.
PN WO2003018621-A2.
PD 06-MAR-2003.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match 12.0%; Score 55.5; DB 7; Length 892;
Best Local Similarity 25.9%; Pred. No. 3.1e+03;
RESULT 1038
ID AAW31363 standard; protein; 955 AA.
DE Cell membrane proton-ATPase.
PN JP09252786-A.
PD 30-SEP-1997.
PA (ORIY) ORIENTAL YEAST CO LTD.
Query Match 12.0%; Score 55.5; DB 2; Length 955;
Best Local Similarity 25.3%; Pred. No. 3.4e+03;
RESULT 1039
ID ADD01181 standard; protein; 1004 AA.
DE Human nucleic acid-associated protein NAAP-19 SEQ ID NO:19.
PN WO2003054219-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 12.0%; Score 55.5; DB 7; Length 1004;
Best Local Similarity 34.8%; Pred. No. 3.7e+03;
RESULT 1040
ID ABR43214 standard; protein; 1027 AA.
DE Human IRAP-10 protein SEQ ID NO:10.
PN WO2003025542-A2.
PD 27-MAR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 12.0%; Score 55.5; DB 6; Length 1027;
Best Local Similarity 29.4%; Pred. No. 3.8e+03;
RESULT 1041
ID ADH42465 standard; protein; 1058 AA.
DE Novel human protein NOV689.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.0%; Score 55.5; DB 8; Length 1058;
Best Local Similarity 25.0%; Pred. No. 4e+03;
RESULT 1042

ID ADJ35096 standard; protein; 1323 AA.
DE Xylanase from an environmental sample seq id 312.
PN WO2003108654-A2.
PD 24-DEC-2003.
PA (DIVE-) DIVERSA CORP.
Query Match 12.0%; Score 55.5; DB 8; Length 1323;
Best Local Similarity 31.2%; Pred. No. 5.4e+03;
RESULT 1043
ID ABR83539 standard; protein; 1524 AA.
DE Human fatty acid CoA ligase-like AMP-binding enzyme SEQ ID NO:2.
PN WO2003057867-A2.
PD 17-JUL-2003.
PA (FARB-) BAYER AG.
Query Match 12.0%; Score 55.5; DB 7; Length 1524;
Best Local Similarity 29.2%; Pred. No. 6.6e+03;
RESULT 1044
ID ADH42473 standard; protein; 1574 AA.
DE Novel human protein NOV68k.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.0%; Score 55.5; DB 8; Length 1574;
Best Local Similarity 25.0%; Pred. No. 6.9e+03;
RESULT 1045
ID ADH42463 standard; protein; 1576 AA.
DE Novel human protein NOV68f.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.0%; Score 55.5; DB 8; Length 1576;
Best Local Similarity 25.0%; Pred. No. 6.9e+03;
RESULT 1046
ID ADH42461 standard; protein; 1576 AA.
DE Novel human protein NOV68e.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.0%; Score 55.5; DB 8; Length 1576;
Best Local Similarity 25.0%; Pred. No. 6.9e+03;
RESULT 1047
ID ABR96136 standard; protein; 1593 AA.
DE Human NOV6a protein SEQ ID NO:14.
PN WO200290568-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
Query Match 12.0%; Score 55.5; DB 6; Length 1593;
Best Local Similarity 25.0%; Pred. No. 7e+03;
RESULT 1048
ID ADN3999 standard; protein; 1593 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C369.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 12.0%; Score 55.5; DB 7; Length 1593;
Best Local Similarity 25.0%; Pred. No. 7e+03;
RESULT 1049
ID ADH42453 standard; protein; 1593 AA.
DE Novel human protein NOV68a.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.0%; Score 55.5; DB 8; Length 1593;
Best Local Similarity 25.0%; Pred. No. 7e+03;
RESULT 1050
ID ADI35778 standard; protein; 1593 AA.
DE Human ADAMTS-12 protein SEQ ID NO:1.
PN WO2003103478-A2.
PD 18-DEC-2003.
PA (ATHE-) ATERSYS INC.
Query Match 12.0%; Score 55.5; DB 8; Length 1593;
Best Local Similarity 25.0%; Pred. No. 7e+03;
RESULT 1051
ID ABB65734 standard; protein; 2050 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 23994.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 12.0%; Score 55.5; DB 4; Length 2050;
Best Local Similarity 26.8%; Pred. No. 1e+04;
RESULT 1052
ID AAG66005 standard; protein; 3241 AA.
DE F. necrophorum leukotoxin protein.
PN WO2003180886-A2.
PD 01-NOV-2001.
PA (UNIV-) UNIV KANSAS STATE RES FOUND.
Query Match 12.0%; Score 55.5; DB 5; Length 3241;
Best Local Similarity 33.3%; Pred. No. 1.9e+04;
RESULT 1053
ID ADI27173 standard; protein; 4660 AA.
DE Rat LRP binding family protein #4.
PN WO2003106657-A2.
PD 24-DEC-2003.
PA (STOW-) STOWERS INST MEDICAL RES.
Query Match 12.0%; Score 55.5; DB 8; Length 4660;
Best Local Similarity 22.2%; Pred. No. 3.1e+04;
RESULT 1054
ID ADK36199 standard; protein; 109 AA.
DE Novel human polypeptide SeqID8281.
PN WO200216439-A2.
PD 28-FEB-2002.
PA (HYSE-) HYSEQ INC.
Query Match 11.9%; Score 55; DB 5; Length 109;
Best Local Similarity 25.0%; Pred. No. 1.9e+02;
RESULT 1055
ID ABP63669 standard; protein; 126 AA.
DE Human ORF39.
PN US2002082206-A1.
PD 27-JUN-2002.
PA (LEAC-) LEACH M D.
PA (MEHR-) MEHRABAN F.
PA (CONL-) CONLEY P B.
PA (TOPP-) TOPPER J N.
PA (LAWD-) LAW D.
Query Match 11.9%; Score 55; DB 5; Length 126;
Best Local Similarity 36.6%; Pred. No. 2.3e+02;
RESULT 1056
ID ABP72618 standard; protein; 131 AA.
DE Snowdrop agglutinin-Manduca sexta allatostatin protein fusion.
PN WO2003014150-A2.
PD 20-FEB-2003.
PA (UYDU-) UNIV DURHAM.
PA (ENVI-) DEPT ENVIRONMENT FOOD & RURAL AFFAIRS.
Query Match 11.9%; Score 55; DB 6; Length 131;
Best Local Similarity 28.1%; Pred. No. 2.4e+02;
RESULT 1057
ID AAU48714 standard; protein; 137 AA.
DE Propionibacterium acnes immunogenic protein #9610.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 11.9%; Score 55; DB 4; Length 137;
Best Local Similarity 41.7%; Pred. No. 2.6e+02;
RESULT 1058
ID ABM45233 standard; protein; 137 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #9909.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 11.9%; Score 55; DB 6; Length 137;
Best Local Similarity 41.7%; Pred. No. 2.6e+02;
RESULT 1059
ID AAB01484 standard; protein; 141 AA.
DE Lentin polypeptide.
PN WO200044780-A1.
PD 03-AUG-2000.
PA (AURE-) AUSTRALIAN RED CROSS BLOOD SERVICE.

Query Match 11.9%; Score 55; DB 3; Length 141;
Best Local Similarity 28.1%; Pred. No. 2.7e+02;
RESULT 1060
ID AAB43074 standard; protein; 145 AA.
DE Human ORFX ORF2838 polypeptide sequence SEQ ID NO:5676.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 11.9%; Score 55; DB 3; Length 145;
Best Local Similarity 30.2%; Pred. No. 2.8e+02;
RESULT 1061
ID ADM74776 standard; protein; 151 AA.
DE Zg-lectin protein related protein sequence, GNA.
PN CN1459503-A.
PD 03-DEC-2003.
PA (UYFU-) UNIV FUDAN.
Query Match 11.9%; Score 55; DB 8; Length 151;
Best Local Similarity 28.1%; Pred. No. 3e+02;
RESULT 1062
ID AAR21742 standard; protein; 157 AA.
DE LECGNA2.
PN WO9202139-A.
PD 20-FEB-1992.
PA (AGRI-) AGRIC GENETICS CO L.
Query Match 11.9%; Score 55; DB 2; Length 157;
Best Local Similarity 28.1%; Pred. No. 3.1e+02;
RESULT 1063
ID AAR83111 standard; protein; 157 AA.
DE Snowdrop lectin LECGNA2.
PN WO9526634-A1.
PD 12-OCT-1995.
PA (AXIS-) AXIS GENETICS LTD.
Query Match 11.9%; Score 55; DB 2; Length 157;
Best Local Similarity 28.1%; Pred. No. 3.1e+02;
RESULT 1064
ID ABB77089 standard; protein; 160 AA.
DE Snowdrop agglutinin.
PN CN1327053-A.
PD 19-DEC-2001.
PA (MICR-) INST MICROBIOLOGY CHINESE ACAD SCI.
Query Match 11.9%; Score 55; DB 5; Length 160;
Best Local Similarity 28.1%; Pred. No. 3.2e+02;
RESULT 1065
ID ABP66205 standard; protein; 163 AA.
DE Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:949.
PN EP127152-A1.
PD 31-JUL-2002.
PA (NEST-) SOC PROD NESTLE SA.
Query Match 11.9%; Score 55; DB 5; Length 163;
Best Local Similarity 26.4%; Pred. No. 3.3e+02;
RESULT 1066
ID AAR48595 standard; protein; 167 AA.
DE Myelin basic protein.
PN WO9404121-A1.
PD 03-MAR-1994.
PA (AUTO-) AUTOIMMUNE INC.
Query Match 11.9%; Score 55; DB 2; Length 167;
Best Local Similarity 24.2%; Pred. No. 3.4e+02;
RESULT 1067
ID ADH88717 standard; protein; 194 AA.
DE Enterococcus faecalis polypeptide #3197.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 11.9%; Score 55; DB 7; Length 194;
Best Local Similarity 37.3%; Pred. No. 4.2e+02;
RESULT 1068
ID AAG29262 standard; protein; 212 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 34786.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 11.9%; Score 55; DB 3; Length 212;
Best Local Similarity 25.3%; Pred. No. 8.5e+02;
RESULT 1078

Best Local Similarity 26.6%; Pred. No. 4.8e+02;
RESULT 1069
ID ABP00552 standard; protein; 225 AA.
DE Human ORFX protein sequence SEQ ID NO:1086.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match 11.9%; Score 55; DB 5; Length 225;
Best Local Similarity 31.9%; Pred. No. 5.2e+02;
RESULT 1070
ID AAG29261 standard; protein; 231 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 34785.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 11.9%; Score 55; DB 3; Length 231;
Best Local Similarity 26.8%; Pred. No. 5.4e+02;
RESULT 1071
ID AAG91725 standard; protein; 232 AA.
DE C glutamicum protein fragment SEQ ID NO: 5479.
PN EP1108790-A2.
PD 20-JUN-2001.
PA (KIOW) KIOWA HAKKO KOGYO KK.
Query Match 11.9%; Score 55; DB 4; Length 232;
Best Local Similarity 27.3%; Pred. No. 5.4e+02;
RESULT 1072
ID AAU25462 standard; protein; 256 AA.
DE Human mdt protein from clone LI:334386.1:2000MAY01.
PN WO200162922-A2.
PD 30-AUG-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 11.9%; Score 55; DB 4; Length 256;
Best Local Similarity 23.9%; Pred. No. 6.2e+02;
RESULT 1073
ID ABR58608 standard; protein; 256 AA.
DE Human cancer related protein SEQ ID NO:265.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 11.9%; Score 55; DB 6; Length 256;
Best Local Similarity 34.4%; Pred. No. 6.2e+02;
RESULT 1074
ID ADH85839 standard; protein; 278 AA.
DE Enterococcus faecalis polypeptide #319.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 11.9%; Score 55; DB 7; Length 278;
Best Local Similarity 30.3%; Pred. No. 7e+02;
RESULT 1075
ID ABB65204 standard; protein; 285 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 22404.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 11.9%; Score 55; DB 4; Length 285;
Best Local Similarity 32.6%; Pred. No. 7.2e+02;
RESULT 1076
ID ABB55312 standard; protein; 314 AA.
DE Lactococcus lactis protein yudG.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 11.9%; Score 55; DB 5; Length 314;
Best Local Similarity 34.8%; Pred. No. 8.3e+02;
RESULT 1077
ID AAG50958 standard; protein; 320 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 64628.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 11.9%; Score 55; DB 3; Length 320;
Best Local Similarity 25.3%; Pred. No. 8.5e+02;
RESULT 1078

ID AAG50957 standard; protein; 324 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 64627.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 11.9%; Score 55; DB 3; Length 324;
Best Local Similarity 25.3%; Pred. No. 8.7e+02;
RESULT 1079
ID AAG07819 standard; protein; 332 AA.
DE Novel human diagnostic protein #7810.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.9%; Score 55; DB 4; Length 332;
Best Local Similarity 35.7%; Pred. No. 9e+02;
RESULT 1080
ID AAG2087 standard; protein; 347 AA.
DE S. epidermidis open reading frame protein sequence SEQ ID NO:1268.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 11.9%; Score 55; DB 4; Length 347;
Best Local Similarity 27.7%; Pred. No. 9.6e+02;
RESULT 1081
ID AAG81684 standard; protein; 347 AA.
DE S. epidermidis open reading frame protein sequence SEQ ID NO:462.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 11.9%; Score 55; DB 4; Length 347;
Best Local Similarity 27.7%; Pred. No. 9.6e+02;
RESULT 1082
ID ABP40647 standard; protein; 351 AA.
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5492.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 11.9%; Score 55; DB 5; Length 351;
Best Local Similarity 27.7%; Pred. No. 9.7e+02;
RESULT 1083
ID AAG31823 standard; protein; 359 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 38281.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 11.9%; Score 55; DB 3; Length 359;
Best Local Similarity 21.4%; Pred. No. 1e+03;
RESULT 1084
ID ABU35189 standard; protein; 359 AA.
DE Protein encoded by Prokaryotic essential gene #20716.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.9%; Score 55; DB 6; Length 359;
Best Local Similarity 25.9%; Pred. No. 1e+03;
RESULT 1085
ID ADH54603 standard; protein; 369 AA.
DE Mouse biglycan protein.
PN US2003148351-A1.
PD 07-AUG-2003.
PA (HENR/) HENRY S P.
PA (HOOK/) HOOK A O M.
PA (MAYN/) WAYNE R.
Query Match 11.9%; Score 55; DB 7; Length 369;
Best Local Similarity 32.7%; Pred. No. 1e+03;
RESULT 1086
ID AAG31822 standard; protein; 375 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 38280.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 11.9%; Score 55; DB 3; Length 375;
Best Local Similarity 21.4%; Pred. No. 1.1e+03;
RESULT 1087
ID AAG31821 standard; protein; 385 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 38279.

PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 11.9%; Score 55; DB 3; Length 385;
Best Local Similarity 21.4%; Pred. No. 1.1e+03;
RESULT 1088
ID AAG42055 standard; protein; 389 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52400.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 11.9%; Score 55; DB 3; Length 389;
Best Local Similarity 25.3%; Pred. No. 1.1e+03;
RESULT 1089
ID AAR13163 standard; protein; 391 AA.
DE Glucose isomerase mutants.
PN EP436502-A.
PD 10-JUL-1991.
PA (KONN) GIST-BROCADES NV.
PA (PLBZ) PLANT GENETIC SYSTEMS NV.
PA (GEMV) GENENCOR INT INC.
Query Match 11.9%; Score 55; DB 2; Length 391;
Best Local Similarity 28.8%; Pred. No. 1.1e+03;
RESULT 1090
ID AAG50956 standard; protein; 391 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 64626.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 11.9%; Score 55; DB 3; Length 391;
Best Local Similarity 25.3%; Pred. No. 1.1e+03;
RESULT 1091
ID AAG42054 standard; protein; 393 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52399.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 11.9%; Score 55; DB 3; Length 393;
Best Local Similarity 25.3%; Pred. No. 1.1e+03;
RESULT 1092
ID ABP98659 standard; protein; 394 AA.
DE Ampullariella sp strain ATCC31351 glucose isomerase.
PN EPI264883-A2.
PD 11-DEC-2002.
PA (GEMV) GENENCOR INT INC.
Query Match 11.9%; Score 55; DB 6; Length 394;
Best Local Similarity 28.8%; Pred. No. 1.1e+03;
RESULT 1093
ID ADJ27188 standard; protein; 400 AA.
DE Human TRICH-20, SEQ ID 20.
PN WO2004013293-A2.
PD 12-FEB-2004.
PA (INCY-) INCYTE CORP.
Query Match 11.9%; Score 55; DB 8; Length 400;
Best Local Similarity 31.5%; Pred. No. 1.2e+03;
RESULT 1094
ID AB084352 standard; protein; 418 AA.
DE Pseudomonas aeruginosa polypeptide #16527.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 11.9%; Score 55; DB 7; Length 418;
Best Local Similarity 29.9%; Pred. No. 1.2e+03;
RESULT 1095
ID AAG42053 standard; protein; 460 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52398.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 11.9%; Score 55; DB 3; Length 460;
Best Local Similarity 25.3%; Pred. No. 1.4e+03;
RESULT 1096
ID ADE31437 standard; protein; 470 AA.
DE Plant yield related protein from clone G1506.
PN WO2003013228-A2.
PD 20-FEB-2003.
PA (MENDE-) MENDEL BIOTECHNOLOGY INC.
Query Match 11.9%; Score 55; DB 7; Length 470;

Best Local Similarity 25.3%; Pred. No. 1.5e+03;
RESULT 1097
ID ADI44177 standard; protein; 470 AA.
DE Plant transcription factor related polypeptide #1677.
PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER/) SHERMAN B K.
PA (RIEC/) RIECHMANN J L.
PA (JIAN/) JIANG C.
PA (HEAR/) HEARD J E.
PA (HAAK/) HAAKE V.
PA (CREE/) CREELMAN R A.
PA (RATC/) RATCLIFFE O.
PA (ADAM/) ADAM L J.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J.
PA (BROU/) BROWN P E.
PA (PILG/) FILGRIM M L.
PA (DUBE/) DUBELL A N.
PA (PINE/) PINEDA O.
PA (YUGG/) YU G.
Query Match 11.9%; Score 55; DB 8; Length 470;
Best Local Similarity 25.3%; Pred. No. 1.5e+03;
RESULT 1098
ID ABB52709 standard; protein; 475 AA.
DE Escherichia coli polypeptide SEQ ID NO 817.
PN WO200166572-A2.
PD 13-SEP-2001.
PA (INRM/) INSERM INST NAT SANTE & RECH MEDICALE.
Query Match 11.9%; Score 55; DB 4; Length 475;
Best Local Similarity 25.7%; Pred. No. 1.5e+03;
RESULT 1099
ID ABO69409 standard; protein; 490 AA.
DE Pseudomonas aeruginosa polypeptide #1584.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 11.9%; Score 55; DB 7; Length 490;
Best Local Similarity 27.4%; Pred. No. 1.5e+03;
RESULT 1100
ID ADH12919 standard; protein; 509 AA.
DE Francisella tularensis immunogenic protein 100, SEQ ID NO:100.
PN WO2004003009-A2.
PD 08-JAN-2004.
PA (MINA/) UK SEC FOR DEFENCE.
Query Match 11.9%; Score 55; DB 8; Length 509;
Best Local Similarity 25.8%; Pred. No. 1.6e+03;
RESULT 1101
ID ADE54724 standard; protein; 575 AA.
DE Rat Protein AAC33823, SEQ ID NO 529.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHEO/) GEN HOSPITAL CORP.
PA (FARB/) BAYER AG.
Query Match 11.9%; Score 55; DB 7; Length 575;
Best Local Similarity 34.2%; Pred. No. 1.9e+03;
RESULT 1102
ID ABO67416 standard; protein; 594 AA.
DE Klebsiella pneumoniae polypeptide seqid 13933.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 11.9%; Score 55; DB 7; Length 594;
Best Local Similarity 23.2%; Pred. No. 2e+03;
RESULT 1103
ID ABB58276 standard; protein; 595 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 1620.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE/) PE CORP NY.
Query Match 11.9%; Score 55; DB 4; Length 595;
Best Local Similarity 25.0%; Pred. No. 2e+03;
RESULT 1104

ID ADB64375 standard; protein; 657 AA.
DE Human protein encoded by clone FCBBF30194550.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 11.9%; Score 55; DB 7; Length 657;
Best Local Similarity 23.9%; Pred. No. 2.3e+03;
RESULT 1105
ID AAY74600 standard; protein; 660 AA.
DE Neisseria gonorrhoeae ORF 163 protein sequence SEQ ID NO:674.
PN WO9557280-A2.
PD 11-NOV-1999.
PA (CHIR/) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Query Match 11.9%; Score 55; DB 3; Length 660;
Best Local Similarity 27.3%; Pred. No. 2.4e+03;
RESULT 1106
ID AAY74601 standard; protein; 660 AA.
DE Neisseria meningitidis ORF 163 protein sequence SEQ ID NO:676.
PN WO9557280-A2.
PD 11-NOV-1999.
PA (CHIR/) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Query Match 11.9%; Score 55; DB 3; Length 660;
Best Local Similarity 27.3%; Pred. No. 2.4e+03;
RESULT 1107
ID AAY74602 standard; protein; 660 AA.
DE Neisseria meningitidis ORF 163 protein sequence SEQ ID NO:678.
PN WO9557280-A2.
PD 11-NOV-1999.
PA (CHIR/) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Query Match 11.9%; Score 55; DB 3; Length 660;
Best Local Similarity 27.3%; Pred. No. 2.4e+03;
RESULT 1108
ID ABU23799 standard; protein; 665 AA.
DE Protein encoded by Prokaryotic essential gene #9326.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.9%; Score 55; DB 6; Length 665;
Best Local Similarity 28.0%; Pred. No. 2.4e+03;
RESULT 1109
ID ABG25624 standard; protein; 671 AA.
DE Novel human diagnostic protein #25615.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.9%; Score 55; DB 4; Length 671;
Best Local Similarity 25.6%; Pred. No. 2.4e+03;
RESULT 1110
ID ABG25989 standard; protein; 671 AA.
DE Novel human diagnostic protein #25980.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.9%; Score 55; DB 4; Length 671;
Best Local Similarity 25.6%; Pred. No. 2.4e+03;
RESULT 1111
ID ABG25081 standard; protein; 671 AA.
DE Novel human diagnostic protein #25072.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.9%; Score 55; DB 4; Length 671;
Best Local Similarity 25.6%; Pred. No. 2.4e+03;
RESULT 1112
ID AAR05701 standard; protein; 673 AA.
DE Human carbastatin polypeptide.
PN JP02056498-A.
PD 26-FEB-1990.
PA (TAKI/) TAKARA SHUZO CO LTD.

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Query Match
Best Local Similarity 11.9%; Score 55; DB 2; Length 673;
RESULT 1113
ID ABR43200 standard; protein; 844 AA.
DE Human REMAP-32 protein SEQ ID NO:32.
PN WO2003025130-A2.
DE Neisseria cell surface polypeptide #12.
PN WO200216612-A2.
PD 28-FEB-2002.
PA (MICR-) MICROSCIENCE LTD.
Query Match
Best Local Similarity 11.9%; Score 55; DB 5; Length 675;
RESULT 1114
ID ABR78636 standard; protein; 675 AA.
DE N. gonorrhoeae amino acid sequence SEQ ID 3802.
PN WO200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Query Match
Best Local Similarity 11.9%; Score 55; DB 6; Length 675;
RESULT 1115
ID ABR97453 standard; protein; 743 AA.
DE Novel human protein SEQ ID NO: 721.
PN WO200222660-A2.
PD 21-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 11.9%; Score 55; DB 5; Length 743;
RESULT 1116
ID ABR74043 standard; protein; 759 AA.
DE Candida albicans essential protein SEQ ID NO 7980.
PN WO200253728-A2.
PD 11-JUN-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 11.9%; Score 55; DB 5; Length 759;
RESULT 1117
ID ADF75087 standard; protein; 819 AA.
DE A. gossypii protein essential for fungal growth & development SeqID 28.
PN WO2003072706-A2.
PD 04-SEP-2003.
PA (SYGN-) SYNGENTA PARTICIPATIONS AG.
Query Match
Best Local Similarity 11.9%; Score 55; DB 7; Length 819;
RESULT 1118
ID ABR43183 standard; protein; 821 AA.
DE Human REMAP-15 protein SEQ ID NO:15.
PN WO2003025130-A2.
PD 27-MAR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 11.9%; Score 55; DB 6; Length 821;
RESULT 1119
ID ABR92061 standard; protein; 824 AA.
DE Human receptors and membrane associated protein REMAP-4.
PN WO200263006-A2.
PD 15-AUG-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 11.9%; Score 55; DB 5; Length 824;
RESULT 1120
ID ADM60377 standard; protein; 829 AA.
DE B. licheniformis sporulation related polypeptide, seq id 49.
PN WO2003087148-A2.
PD 23-OCT-2003.
PA (NOVO-) NOVOZYMES AS.
Query Match
Best Local Similarity 11.9%; Score 55; DB 8; Length 829;
RESULT 1121
ID AAG43632 standard; protein; 835 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 54558.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 11.9%; Score 55; DB 3; Length 835;
RESULT 1122
ID ABR43200 standard; protein; 844 AA.
DE Human REMAP-32 protein SEQ ID NO:32.
PN WO2003025130-A2.
DE Neisseria cell surface polypeptide #12.
PN WO200216612-A2.
PD 28-FEB-2002.
PA (MICR-) MICROSCIENCE LTD.
Query Match
Best Local Similarity 11.9%; Score 55; DB 6; Length 844;
RESULT 1123
ID ABR43631 standard; protein; 845 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 54557.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 11.9%; Score 55; DB 3; Length 845;
RESULT 1124
ID ABR93794 standard; protein; 853 AA.
DE Herbicidically active polypeptide SEQ ID NO 3005.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB-) BAYER AG.
Query Match
Best Local Similarity 11.9%; Score 55; DB 5; Length 853;
RESULT 1125
ID AAR29815 standard; protein; 855 AA.
DE S receptor kinase protein SRK2.
PN EP519869-A2.
PD 23-DEC-1992.
PA (CIBA-) CIBA GEIGY AG.
PA (NOVS-) NOVARTIS AG.
Query Match
Best Local Similarity 11.9%; Score 55; DB 2; Length 855;
RESULT 1126
ID ABR48139 standard; protein; 863 AA.
DE Protein encoded by Prokaryotic essential gene #33666.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 11.9%; Score 55; DB 6; Length 863;
RESULT 1127
ID ABR4702 standard; protein; 883 AA.
DE Protein encoded by Prokaryotic essential gene #229.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 11.9%; Score 55; DB 6; Length 883;
RESULT 1128
ID AAG43630 standard; protein; 923 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 54556.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 11.9%; Score 55; DB 3; Length 923;
RESULT 1129
ID ABR63047 standard; protein; 952 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 15933.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match
Best Local Similarity 11.9%; Score 55; DB 4; Length 952;
RESULT 1130
ID ABR31785 standard; protein; 986 AA.
DE Human ankyrin 4 polypeptide.
PN CN1293251-A.
PD 02-MAY-2001.
PA (SHEN-) SHENGYUAN GENE DEV CO LTD SHANGHAI.
Query Match
Best Local Similarity 11.9%; Score 55; DB 4; Length 986;
RESULT 1131
ID ADF07451 standard; protein; 1036 AA.
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DE Bacterial polypeptide #3564.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 11.9%; Score 55; DB 7; Length 1036;
Best Local Similarity 26.4%; Pred. No. 4.4e+03;
RESULT 1132
ID ADO44171 standard; protein; 1059 AA.
DE Structural and cytoskeleton-associated polypeptide #7.
PN WO2004029205-A2.
PD 08-APR-2004.
PA (INCY-) INCYTE CORP.
Query Match 11.9%; Score 55; DB 8; Length 1059;
Best Local Similarity 28.6%; Pred. No. 4.6e+03;
RESULT 1133
ID ADC39122 standard; protein; 1139 AA.
DE Novel human NOVX polypeptide SEQ ID NO: 64.
PN WO2003010327-A2.
PD 06-FEB-2003.
PA (CURA-) CURAGEN CORP.
Query Match 11.9%; Score 55; DB 7; Length 1139;
Best Local Similarity 23.9%; Pred. No. 5.1e+03;
RESULT 1134
ID ADF13896 standard; protein; 1180 AA.
DE Human endometrial-specific protein - SEQ ID 527.
PN WO2003059927-A1.
PD 24-JUL-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 11.9%; Score 55; DB 7; Length 1180;
Best Local Similarity 30.8%; Pred. No. 5.3e+03;
RESULT 1135
ID ADC30931 standard; protein; 1223 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1013.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 11.9%; Score 55; DB 7; Length 1223;
Best Local Similarity 22.2%; Pred. No. 5.6e+03;
RESULT 1136
ID ABB60352 standard; protein; 1225 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 7848.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 11.9%; Score 55; DB 4; Length 1225;
Best Local Similarity 27.8%; Pred. No. 5.8e+03;
RESULT 1137
ID AAO26231 standard; protein; 1250 AA.
DE MDDT related human protein SEQ ID No 9.
PN WO200296951-A1.
PD 05-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 11.9%; Score 55; DB 6; Length 1250;
Best Local Similarity 25.0%; Pred. No. 5.8e+03;
RESULT 1138
ID AAE33667 standard; protein; 1250 AA.
DE Human structural and cytoskeleton-associated protein (SCAP) #1.
PN WO200201009-A2.
PD 19-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 11.9%; Score 55; DB 6; Length 1250;
Best Local Similarity 23.9%; Pred. No. 5.8e+03;
RESULT 1139
ID ADM87156 standard; protein; 1250 AA.
DE Human protein SEQ ID NO:249.
PN WO2004009834-A2.
PD 29-JAN-2004.
PA (NUVE-) NUVELO INC.
Query Match 11.9%; Score 55; DB 8; Length 1250;
Best Local Similarity 25.0%; Pred. No. 5.8e+03;
RESULT 1140
ID AAR88469 standard; protein; 1464 AA.
DE Feline infectious peritonitis 1 virus spike protein.

PN JP07327683-A.
PD 19-DEC-1995.
PA (KITA) KITASATO KENKYUSHO SH.
Query Match 11.9%; Score 55; DB 2; Length 1464;
Best Local Similarity 28.8%; Pred. No. 7.2e+03;
RESULT 1141
ID ABB71141 standard; protein; 1833 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 40215.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 11.9%; Score 55; DB 4; Length 1833;
Best Local Similarity 24.6%; Pred. No. 9.9e+03;
RESULT 1142
ID ASU15806 standard; protein; 1953 AA.
DE Protein encoded by Prokaryotic essential gene #1333.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.9%; Score 55; DB 6; Length 1953;
Best Local Similarity 24.8%; Pred. No. 1.1e+04;
RESULT 1143
ID ABU38191 standard; protein; 2273 AA.
DE Protein encoded by Prokaryotic essential gene #23718.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.9%; Score 55; DB 6; Length 2273;
Best Local Similarity 28.3%; Pred. No. 1.3e+04;
RESULT 1144
ID AAP81771 standard; protein; 3210 AA.
DE Deduced sequence encoded by bottom reading frame of cDNA clone HIV-2
DE SBL/ISY of HIV related retrovirus strain.
PN WO8808449-A.
PD 03-NOV-1988.
PA (SBL-) SBL STATENS BAKTERIOLOGISKA LAB.
PA (STAT-) STATENS BAKTERIOLOGISKA LAB.
Query Match 11.9%; Score 55; DB 1; Length 3210;
Best Local Similarity 29.4%; Pred. No. 2.2e+04;
RESULT 1145
ID ADI26356 standard; protein; 76 AA.
DE Fusarium graminearum partial polyketide synthetase SEQ ID NO:8.
PN WO2004005522-A2.
PD 15-JAN-2004.
PA (BADI) BASF AG.
Query Match 11.8%; Score 54.5; DB 8; Length 76;
Best Local Similarity 31.7%; Pred. No. 1.3e+02;
RESULT 1146
ID ABB11339 standard; peptide; 87 AA.
DE Human beta-fibrinogen homologue, SEQ ID NO:1709.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.8%; Score 54.5; DB 4; Length 87;
Best Local Similarity 36.4%; Pred. No. 1.6e+02;
RESULT 1147
ID AAM50527 standard; protein; 115 AA.
DE Plasmodium falciparum MSP-1 peptide p115MSP-1.
PN WO200185927-A1.
PD 15-NOV-2001.
PA (GEQU) UNIV GEORGETOWN.
Query Match 11.8%; Score 54.5; DB 5; Length 115;
Best Local Similarity 31.6%; Pred. No. 2.3e+02;
RESULT 1148
ID ADI39518 standard; protein; 177 AA.
DE Arabidopsis thaliana DIMIC related protein #3.
PN WO200253589-A2.
PD 11-JUL-2002.
PA (CROP-) CROPDESIGN NV.
Query Match 11.8%; Score 54.5; DB 5; Length 177;
Best Local Similarity 31.9%; Pred. No. 4.3e+02;
RESULT 1149

ID AAE29348 standard; protein; 220 AA.
DE Plasmodium falciparum MSP138-N-terminal domain protein.
PN WO200270542-A2.
PD 12-SEP-2002.
PA (SBLI-) ST ELIZABETH'S MEDICAL CENT INC.
Query Match 11.8%; Score 54.5; DB 5; Length 220;
Best Local Similarity 31.6%; Pred. No. 5.8e+02;
RESULT 1150
ID ADC94581 standard; protein; 256 AA.
DE E. faecium protein sequence SEQ ID 4208.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 11.8%; Score 54.5; DB 7; Length 256;
Best Local Similarity 23.2%; Pred. No. 7.2e+02;
RESULT 1151
ID ABU05566 standard; protein; 257 AA.
DE M. tuberculosis and M. leprae marker protein #217.
PN WO200274903-A2.
PD 26-SEP-2002.
PA (INSP) INST PASTEUR.
Query Match 11.8%; Score 54.5; DB 5; Length 257;
Best Local Similarity 42.5%; Pred. No. 7.2e+02;
RESULT 1152
ID ABM70758 standard; protein; 260 AA.
DE Photorhabdus luminescens protein sequence #3855.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
Query Match 11.8%; Score 54.5; DB 6; Length 260;
Best Local Similarity 40.0%; Pred. No. 7.3e+02;
RESULT 1153
ID ADI39482 standard; protein; 268 AA.
DE Arabidopsis thaliana DIM1 interacting molecule 70A (DIMIC70A) protein.
PN WO200253589-A2.
PD 11-JUL-2002.
PA (CROP-) CROPDISEGN NV.
Query Match 11.8%; Score 54.5; DB 5; Length 268;
Best Local Similarity 31.9%; Pred. No. 7.7e+02;
RESULT 1154
ID ABU35646 standard; protein; 268 AA.
DE Protein encoded by Prokaryotic essential gene #21173.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.8%; Score 54.5; DB 6; Length 268;
Best Local Similarity 35.4%; Pred. No. 7.7e+02;
RESULT 1155
ID ADI39483 standard; protein; 269 AA.
DE Arabidopsis thaliana DIM1 interacting molecule 70B (DIMIC70B) protein.
PN WO200253589-A2.
PD 11-JUL-2002.
PA (CROP-) CROPDISEGN NV.
Query Match 11.8%; Score 54.5; DB 5; Length 269;
Best Local Similarity 31.9%; Pred. No. 7.7e+02;
RESULT 1156
ID ABG05901 standard; protein; 280 AA.
DE Novel human diagnostic protein #5892.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.8%; Score 54.5; DB 4; Length 280;
Best Local Similarity 34.3%; Pred. No. 8.1e+02;
RESULT 1157
ID ABU25762 standard; protein; 290 AA.
DE Protein encoded by Prokaryotic essential gene #11289.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.8%; Score 54.5; DB 6; Length 290;
Best Local Similarity 28.6%; Pred. No. 8.6e+02;
RESULT 1158

ID ABG77226 standard; protein; 294 AA.
DE Selected Interacting Domain (SID) polypeptide #37.
PN WO200259255-A2.
PD 01-AUG-2002.
PA (HYBR-) HYBRIGENICS.
Query Match 11.8%; Score 54.5; DB 5; Length 294;
Best Local Similarity 25.3%; Pred. No. 8.7e+02;
RESULT 1159
ID ABU11097 standard; protein; 294 AA.
DE Yeast selected interacting domain protein SEQ ID NO: 328.
PN WO200266504-A2.
PD 29-AUG-2002.
PA (HYBR-) HYBRIGENICS.
Query Match 11.8%; Score 54.5; DB 5; Length 294;
Best Local Similarity 25.3%; Pred. No. 8.7e+02;
RESULT 1160
ID AAG17007 standard; protein; 311 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 17865.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (HYSE-) HYSEQ INC.
Query Match 11.8%; Score 54.5; DB 3; Length 311;
Best Local Similarity 41.7%; Pred. No. 9.4e+02;
RESULT 1161
ID AAU29754 standard; protein; 313 AA.
DE Novel human secreted protein #245.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.8%; Score 54.5; DB 4; Length 313;
Best Local Similarity 26.4%; Pred. No. 9.5e+02;
RESULT 1162
ID ABU18150 standard; protein; 313 AA.
DE Protein encoded by Prokaryotic essential gene #3677.
PN WO200277193-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.8%; Score 54.5; DB 6; Length 313;
Best Local Similarity 31.7%; Pred. No. 9.5e+02;
RESULT 1163
ID ABG22917 standard; protein; 315 AA.
DE Novel human diagnostic protein #22908.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.8%; Score 54.5; DB 4; Length 315;
Best Local Similarity 25.6%; Pred. No. 9.6e+02;
RESULT 1164
ID ADG22560 standard; protein; 316 AA.
DE Cyanophage S-2L encoded protein #305.
PN FR2839079-A1.
PD 31-OCT-2003.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
PA (GENO-) GENOSCOPE CENT NAT SEQUENCE GRP INTERE.
Query Match 11.8%; Score 54.5; DB 8; Length 316;
Best Local Similarity 27.8%; Pred. No. 9.6e+02;
RESULT 1165
ID ABG27761 standard; protein; 321 AA.
DE Novel human diagnostic protein #27752.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.8%; Score 54.5; DB 4; Length 321;
Best Local Similarity 26.8%; Pred. No. 9.9e+02;
RESULT 1166
ID AAE14518 standard; protein; 328 AA.
DE Arabidopsis thaliana Earl protein.
PN WO20020903-A2.
PD 03-JAN-2002.
PA (UVRQ) UNIV ROCKEFELLER.
Query Match 11.8%; Score 54.5; DB 5; Length 328;
Best Local Similarity 25.6%; Pred. No. 1e+03;
RESULT 1167

ID AAE14519 standard; protein; 328 AA.
DE Arabidopsis thaliana ESRI-like protein.
PN WO200200903-A2.
PD 03-JAN-2002.
PA (UYRQ) UNIV ROCKFELLER.
Query Match 11.8%; Score 54.5; DB 5; Length 328;
Best Local Similarity 25.6%; Pred. No. 1e+03;
RESULT 1168
ID ABG70898 standard; protein; 328 AA.
DE Arabidopsis enhancer of shoot generation 1, ESRI.
PN US6441276-B1.
PD 27-AUG-2002.
PA (UYRQ) UNIV ROCKFELLER.
Query Match 11.8%; Score 54.5; DB 5; Length 328;
Best Local Similarity 25.6%; Pred. No. 1e+03;
RESULT 1169
ID ADO61813 standard; protein; 328 AA.
DE Transcription factor GL796, SEQ ID 280.
PN WO2004031349-A2.
PD 15-APR-2004.
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
Query Match 11.8%; Score 54.5; DB 8; Length 328;
Best Local Similarity 25.8%; Pred. No. 1e+03;
RESULT 1170
ID AAE29351 standard; protein; 334 AA.
DE Plasmodium falciparum MSP138 (merozoite surface protein 1) protein #2.
PN WO200270542-A2.
PD 12-SEP-2002.
PA (SELI-) ST ELIZABETH'S MEDICAL CENT INC.
Query Match 11.8%; Score 54.5; DB 5; Length 334;
Best Local Similarity 31.6%; Pred. No. 1e+03;
RESULT 1171
ID AAG17006 standard; protein; 338 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 17864.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 11.8%; Score 54.5; DB 3; Length 338;
Best Local Similarity 41.7%; Pred. No. 1.1e+03;
RESULT 1172
ID ABB92433 standard; protein; 343 AA.
DE Herbicidally active polypeptide SEQ ID NO 1644.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 11.8%; Score 54.5; DB 5; Length 343;
Best Local Similarity 20.0%; Pred. No. 1.1e+03;
RESULT 1173
ID AAY03851 standard; protein; 354 AA.
DE Murine nodal protein.
PN WO9909198-A1.
PD 25-FEB-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.8%; Score 54.5; DB 2; Length 354;
Best Local Similarity 33.3%; Pred. No. 1.1e+03;
RESULT 1174
ID ADM05653 standard; protein; 356 AA.
DE Human protein of the invention SEQ ID NO:4338.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 11.8%; Score 54.5; DB 7; Length 356;
Best Local Similarity 37.3%; Pred. No. 1.1e+03;
RESULT 1175
ID AAE29347 standard; protein; 360 AA.
DE Plasmodium falciparum MSP138 (merozoite surface protein 1) protein #1.
PN WO200270542-A2.
PD 12-SEP-2002.
PA (SELI-) ST ELIZABETH'S MEDICAL CENT INC.
Query Match 11.8%; Score 54.5; DB 5; Length 360;
Best Local Similarity 31.8%; Pred. No. 1.2e+03;
RESULT 1176
ID ADC13577 standard; protein; 414 AA.
DE Human NOVX protein, SEQ ID NO 56.

PN WO2003004617-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 11.8%; Score 54.5; DB 7; Length 414;
Best Local Similarity 37.3%; Pred. No. 1.4e+03;
RESULT 1177
ID ABB60805 standard; protein; 425 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 9207.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 11.8%; Score 54.5; DB 4; Length 425;
Best Local Similarity 40.5%; Pred. No. 1.5e+03;
RESULT 1178
ID ADE52963 standard; protein; 434 AA.
DE FEN-1 related polypeptide used within the scope of the invention, #18.
PN WO200270755-A2.
PD 12-SEP-2002.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Query Match 11.8%; Score 54.5; DB 5; Length 434;
Best Local Similarity 22.1%; Pred. No. 1.5e+03;
RESULT 1179
ID ADA66105 standard; protein; 434 AA.
DE DNAP-related protein #11.
PN US2003044796-A1.
PD 06-MAR-2003.
PA (NERI/) NERI B P.
PA (HALL/) HALL J G.
PA (LYAM/) LYAMICHEV V.
PA (SMIT/) SMITH L M.
Query Match 11.8%; Score 54.5; DB 7; Length 434;
Best Local Similarity 22.1%; Pred. No. 1.5e+03;
RESULT 1180
ID ADN01952 standard; protein; 481 AA.
DE Staphylococcus aureus related bacteriophage protein #1.
PN WO2004020635-A1.
PD 11-MAR-2004.
PA (TECH-) TECHNO NETWORK SHIKOKU CO LTD.
Query Match 11.8%; Score 54.5; DB 8; Length 481;
Best Local Similarity 21.5%; Pred. No. 1.7e+03;
RESULT 1181
ID ADN01939 standard; protein; 481 AA.
DE Staphylococcus aureus related bacteriophage protein, SEQ ID 1.
PN WO2004020635-A1.
PD 11-MAR-2004.
PA (TECH-) TECHNO NETWORK SHIKOKU CO LTD.
Query Match 11.8%; Score 54.5; DB 8; Length 481;
Best Local Similarity 21.5%; Pred. No. 1.7e+03;
RESULT 1182
ID AAG26391 standard; protein; 489 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 30829.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 11.8%; Score 54.5; DB 3; Length 489;
Best Local Similarity 23.9%; Pred. No. 1.8e+03;
RESULT 1183
ID AAE23112 standard; protein; 506 AA.
DE Influenza A virus/singapore/1/57/ca NP mutant protein.
PN WO200224876-A2.
PD 28-MAR-2002.
PA (POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.
Query Match 11.8%; Score 54.5; DB 5; Length 506;
Best Local Similarity 29.9%; Pred. No. 1.9e+03;
RESULT 1184
ID ADA56920 standard; protein; 519 AA.
DE Human secreted protein #203.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.8%; Score 54.5; DB 6; Length 519;
Best Local Similarity 28.2%; Pred. No. 1.9e+03;
RESULT 1185
ID ADA40767 standard; protein; 519 AA.

DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.8%; Score 54.5; DB 6; Length 519;
Best Local Similarity 28.2%; Pred. No. 1.9e+03;
RESULT 1186
ID AD74130 standard; protein; 519 AA.
DE Human secreted protein - SEQ ID 763.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.8%; Score 54.5; DB 7; Length 519;
Best Local Similarity 28.2%; Pred. No. 1.9e+03;
RESULT 1187
ID AAY86227 standard; protein; 520 AA.
DE Human secreted protein HFTDL56, SEQ ID NO:142.
PN WO996041-A1.
PD 23-DEC-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.8%; Score 54.5; DB 3; Length 520;
Best Local Similarity 28.2%; Pred. No. 1.9e+03;
RESULT 1188
ID AB053370 standard; protein; 520 AA.
DE Novel human secreted protein #13.
PN US2003065151-A1.
PD 03-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.8%; Score 54.5; DB 6; Length 520;
Best Local Similarity 28.2%; Pred. No. 1.9e+03;
RESULT 1189
ID AB861920 standard; protein; 521 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 12552.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PPEK-) PE CORP NY.
Query Match 11.8%; Score 54.5; DB 4; Length 521;
Best Local Similarity 27.8%; Pred. No. 1.9e+03;
RESULT 1190
ID AAG09309 standard; protein; 533 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 7190.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 11.8%; Score 54.5; DB 3; Length 533;
Best Local Similarity 36.5%; Pred. No. 2e+03;
RESULT 1191
ID AAG52378 standard; protein; 547 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 66574.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 11.8%; Score 54.5; DB 3; Length 547;
Best Local Similarity 36.5%; Pred. No. 2.1e+03;
RESULT 1192
ID AB021139 standard; protein; 551 AA.
DE Protein encoded by Prokaryotic essential gene #6666.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.8%; Score 54.5; DB 6; Length 551;
Best Local Similarity 29.5%; Pred. No. 2.1e+03;
RESULT 1193
ID AAG09308 standard; protein; 560 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 7189.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 11.8%; Score 54.5; DB 3; Length 560;
Best Local Similarity 36.5%; Pred. No. 2.2e+03;
RESULT 1194
ID AAG52377 standard; protein; 573 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 66573.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 11.8%; Score 54.5; DB 3; Length 573;

Best Local Similarity 36.5%; Pred. No. 2.2e+03;
RESULT 1195
ID AAB49986 standard; protein; 587 AA.
DE P. gallinaceum chitinase SEQ ID NO: 4.
PN WO200073488-A1.
PD 07-DEC-2000.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 11.8%; Score 54.5; DB 4; Length 587;
Best Local Similarity 26.7%; Pred. No. 2.3e+03;
RESULT 1196
ID ABB54353 standard; protein; 592 AA.
DE Lactococcus lactis protein p1230.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 11.8%; Score 54.5; DB 5; Length 592;
Best Local Similarity 24.2%; Pred. No. 2.3e+03;
RESULT 1197
ID ADG65702 standard; protein; 592 AA.
DE Mouse transforming growth factor beta (TGF-beta) receptor II.
PN WO2003000656-A2.
PD 03-JAN-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 11.8%; Score 54.5; DB 7; Length 592;
Best Local Similarity 26.3%; Pred. No. 2.3e+03;
RESULT 1198
ID ABJ18979 standard; protein; 645 AA.
DE Pathogen specific antigen related staphylococcal protein SEQ ID NO 142.
PN WO200259148-A2.
PD 01-AUG-2002.
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
Query Match 11.8%; Score 54.5; DB 6; Length 645;
Best Local Similarity 31.9%; Pred. No. 2.6e+03;
RESULT 1199
ID AAW55483 standard; protein; 668 AA.
DE H. pylori ORF 14ap10815_20585777_ci_13 cell envelope OMP.
PN WO9737044-A1.
PD 09-OCT-1997.
PA (ASTR-) ASTRA AB.
Query Match 11.8%; Score 54.5; DB 2; Length 668;
Best Local Similarity 27.9%; Pred. No. 2.8e+03;
RESULT 1200
ID AAB46377 standard; protein; 668 AA.
DE H. pylori HPN137 protein.
PN WO200073502-A2.
PD 07-DEC-2000.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match 11.8%; Score 54.5; DB 4; Length 668;
Best Local Similarity 27.9%; Pred. No. 2.8e+03;
RESULT 1201
ID AAW55328 standard; protein; 677 AA.
DE H. pylori ORF hp3el0349orf27 protein.
PN WO9737044-A1.
PD 09-OCT-1997.
PA (ASTR-) ASTRA AB.
Query Match 11.8%; Score 54.5; DB 2; Length 677;
Best Local Similarity 27.9%; Pred. No. 2.8e+03;
RESULT 1202
ID ABR40766 standard; protein; 707 AA.
DE Glycine max oil trait related protein sequence SEQ ID NO:352.
PN WO2003002751-A2.
PD 09-JAN-2003.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 11.8%; Score 54.5; DB 6; Length 707;
Best Local Similarity 21.2%; Pred. No. 3e+03;
RESULT 1203
ID AAY05753 standard; protein; 721 AA.
DE Streptococcus pneumoniae 79 kDa complement C3-degrading protease.
PN WO9915675-A1.
PD 01-APR-1999.
PA (MINU) UNIV MINNESOTA.

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PA (AMCY ) AMERICAN CYANAMID CO.
  Query Match 11.8%; Score 54.5; DB 2; Length 721;
  Best Local Similarity 26.4%; Pred. No. 3.1e+03;
RESULT 1204
ID AEG93140 standard; protein; 738 AA.
DE S. cerevisiae BAX-associated protein fragment SEQ ID 238.
PN WO200264766-A2.
PD 22-AUG-2002.
PA (JANC ) JANSSEN PHARM NV.
  Query Match 11.8%; Score 54.5; DB 5; Length 738;
  Best Local Similarity 22.9%; Pred. No. 3.2e+03;
RESULT 1205
ID ABB93905 standard; protein; 748 AA.
DE Herbicidally active polypeptide SEQ ID NO 3116.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB ) BAYER AG.
  Query Match 11.8%; Score 54.5; DB 5; Length 748;
  Best Local Similarity 27.1%; Pred. No. 3.2e+03;
RESULT 1206
ID ADN73341 standard; protein; 748 AA.
DE Male cress protein upregulated in E2Fa/Dpa expressing plants SeqID 1236.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDISEIGN NV.
  Query Match 11.8%; Score 54.5; DB 8; Length 748;
  Best Local Similarity 27.1%; Pred. No. 3.2e+03;
RESULT 1207
ID AAW55095 standard; protein; 763 AA.
DE Streptococcus pneumoniae SP0042 protein.
PN WO9818930-A2.
PD 07-MAY-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match 11.8%; Score 54.5; DB 2; Length 763;
  Best Local Similarity 26.4%; Pred. No. 3.3e+03;
RESULT 1208
ID ABP54589 standard; protein; 763 AA.
DE S. pneumoniae SP042 protein sequence SEQ ID NO:66.
PN US2002061545-A1.
PD 23-MAY-2002.
PA (CHOI/) CHOI G H.
PA (KUNS/) KUNSCH C A.
PA (BARA/) BARASH S C.
PA (DILL/) DILLON P J.
PA (DOUG/) DOUGHERTY B.
PA (FANN/) FANNON M R.
PA (ROSE/) ROSEN C A.
  Query Match 11.8%; Score 54.5; DB 5; Length 763;
  Best Local Similarity 26.4%; Pred. No. 3.3e+03;
RESULT 1209
ID ADC45147 standard; protein; 763 AA.
DE S. pneumoniae antigenic protein SP042.
PN US6573082-B1.
PD 03-JUN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match 11.8%; Score 54.5; DB 7; Length 763;
  Best Local Similarity 26.4%; Pred. No. 3.3e+03;
RESULT 1210
ID AAW26727 standard; protein; 764 AA.
DE Yeast Mps1p protein kinase.
PN WO9739143-A2.
PD 23-OCT-1997.
PA (ABBO ) ABBOTT LAB.
PA (UYTB-) UNIV TECHNOLOGY CORP.
  Query Match 11.8%; Score 54.5; DB 2; Length 764;
  Best Local Similarity 25.3%; Pred. No. 3.3e+03;
RESULT 1211
ID ABG27762 standard; protein; 764 AA.
DE Novel human diagnostic protein #27753.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
  Query Match 11.8%; Score 54.5; DB 4; Length 764;
  Best Local Similarity 25.3%; Pred. No. 3.3e+03;
  Best Local Similarity 29.3%; Pred. No. 3.3e+03;
RESULT 1212
ID ABP54947 standard; protein; 764 AA.
DE Saccharomyces cerevisiae protein kinase Mps1.
PN WO200269444-A1.
PD 06-SEP-2002.
PA (CHIR ) CHIRON CORP.
  Query Match 11.8%; Score 54.5; DB 5; Length 764;
  Best Local Similarity 25.3%; Pred. No. 3.3e+03;
RESULT 1213
ID ABU02688 standard; protein; 764 AA.
DE S. pneumoniae type 4 strain protein from coding region #2267.
PN WO200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
  Query Match 11.8%; Score 54.5; DB 6; Length 764;
  Best Local Similarity 26.7%; Pred. No. 3.3e+03;
RESULT 1214
ID ABU61620 standard; protein; 764 AA.
DE Yeast Mps1 protein.
PN US2003045491-A1.
PD 06-MAR-2003.
PA (REIN/) REINHARD C.
PA (JEFF/) JERPERSON A B.
PA (CHAN/) CHAN V W.
  Query Match 11.8%; Score 54.5; DB 7; Length 764;
  Best Local Similarity 25.3%; Pred. No. 3.3e+03;
RESULT 1215
ID ADI60395 standard; protein; 764 AA.
DE Secreted polypeptide encoded by gene splice variant #31.
PN WO2003025142-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
  Query Match 11.8%; Score 54.5; DB 7; Length 764;
  Best Local Similarity 29.3%; Pred. No. 3.3e+03;
RESULT 1216
ID AAB12764 standard; protein; 805 AA.
DE Streptococcus pneumoniae strain JNR7/87 BVH-11 protein antigen.
PN WO200039299-A2.
PD 06-JUL-2000.
PA (BIOC-) BIOCHEM PHARMA INC.
  Query Match 11.8%; Score 54.5; DB 3; Length 805;
  Best Local Similarity 26.4%; Pred. No. 3.6e+03;
RESULT 1217
ID AAB12765 standard; protein; 807 AA.
DE Streptococcus pneumoniae strain SP63 BVH-11 protein antigen.
PN WO200039299-A2.
PD 06-JUL-2000.
PA (BIOC-) BIOCHEM PHARMA INC.
  Query Match 11.8%; Score 54.5; DB 3; Length 807;
  Best Local Similarity 25.3%; Pred. No. 3.6e+03;
RESULT 1218
ID AAB12761 standard; protein; 811 AA.
DE Streptococcus pneumoniae strain WU2 BVH-11 protein antigen.
PN WO200039299-A2.
PD 06-JUL-2000.
PA (BIOC-) BIOCHEM PHARMA INC.
  Query Match 11.8%; Score 54.5; DB 3; Length 811;
  Best Local Similarity 25.3%; Pred. No. 3.6e+03;
RESULT 1219
ID AAB12762 standard; protein; 811 AA.
DE Streptococcus pneumoniae strain A66 BVH-11 protein antigen.
PN WO200039299-A2.
PD 06-JUL-2000.
PA (BIOC-) BIOCHEM PHARMA INC.
  Query Match 11.8%; Score 54.5; DB 3; Length 811;
  Best Local Similarity 25.3%; Pred. No. 3.6e+03;
RESULT 1220
ID AAB12760 standard; protein; 811 AA.
DE Streptococcus pneumoniae strain P4241 BVH-11 protein antigen.
PN WO200039299-A2.
PD 06-JUL-2000.

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PA (BIOC-) BIOCHEM PHARMA INC.
Query Match 11.8%; Score 54.5; DB 3; Length 811;
Best Local Similarity 25.3%; Pred. No. 3.6e+03;
RESULT 1221
ID AAB12763 standard; protein; 811 AA.
DE Streptococcus pneumoniae strain RX1 BVH-11 protein antigen.
PN WO200039299-A2.
PD 06-JUL-2000.
PA (BIOC-) BIOCHEM PHARMA INC.
Query Match 11.8%; Score 54.5; DB 3; Length 811;
Best Local Similarity 25.3%; Pred. No. 3.6e+03;
RESULT 1222
ID AAB12757 standard; protein; 816 AA.
DE Streptococcus pneumoniae strain A66 BVH-11-2 protein antigen.
PN WO200039299-A2.
PD 06-JUL-2000.
PA (BIOC-) BIOCHEM PHARMA INC.
Query Match 11.8%; Score 54.5; DB 3; Length 816;
Best Local Similarity 25.3%; Pred. No. 3.7e+03;
RESULT 1223
ID AAB12756 standard; protein; 816 AA.
DE Streptococcus pneumoniae strain P4241 BVH-11-2 protein antigen.
PN WO200039299-A2.
PD 06-JUL-2000.
PA (BIOC-) BIOCHEM PHARMA INC.
Query Match 11.8%; Score 54.5; DB 3; Length 816;
Best Local Similarity 25.3%; Pred. No. 3.7e+03;
RESULT 1224
ID AAB12754 standard; protein; 819 AA.
DE Streptococcus pneumoniae strain SP64 BVH-11-2 protein antigen.
PN WO200039299-A2.
PD 06-JUL-2000.
PA (BIOC-) BIOCHEM PHARMA INC.
Query Match 11.8%; Score 54.5; DB 3; Length 819;
Best Local Similarity 26.4%; Pred. No. 3.7e+03;
RESULT 1225
ID AAB12740 standard; protein; 819 AA.
DE Streptococcus pneumoniae strain BVH-11-2M protein antigen SEQ ID NO:73.
PN WO200039299-A2.
PD 06-JUL-2000.
PA (BIOC-) BIOCHEM PHARMA INC.
Query Match 11.8%; Score 54.5; DB 3; Length 819;
Best Local Similarity 26.4%; Pred. No. 3.7e+03;
RESULT 1226
ID AAB01469 standard; protein; 819 AA.
DE Recombinant variant of Sp36 (Sp36B) of S. pneumoniae.
PN WO200037105-A2.
PD 29-JUN-2000.
PA (MEDI-) MEDIMMUNE INC.
Query Match 11.8%; Score 54.5; DB 3; Length 819;
Best Local Similarity 26.4%; Pred. No. 3.7e+03;
RESULT 1227
ID AAU84087 standard; peptide; 819 AA.
DE Truncated variant of S. pneumoniae BVH-11-2, BVH-11-2.
PN WO200198334-A2.
PD 27-DEC-2001.
PA (SHIR-) SHIRE BIOCHEM INC.
Query Match 11.8%; Score 54.5; DB 5; Length 819;
Best Local Similarity 26.4%; Pred. No. 3.7e+03;
RESULT 1228
ID ABU01597 standard; protein; 819 AA.
DE S. pneumoniae type 4 strain protein from coding region #1173.
PN WO20027021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 11.8%; Score 54.5; DB 6; Length 819;
Best Local Similarity 26.4%; Pred. No. 3.7e+03;
RESULT 1229
ID ABM18820 standard; protein; 819 AA.
DE S. pneumoniae variant protein BVH-11-2M.
PN WO2003054007-A2.
PD 03-JUL-2003.

PA (SHIR-) SHIRE BIOCHEM INC.
Query Match 11.8%; Score 54.5; DB 7; Length 819;
Best Local Similarity 26.4%; Pred. No. 3.7e+03;
RESULT 1230
ID AN92169 standard; protein; 819 AA.
DE S. pneumoniae antigenic protein sequence SeqID366.
PN WO2004020609-A2.
PD 11-MAR-2004.
PA (TUFT) UNIV TUFTS.
Query Match 11.8%; Score 54.5; DB 8; Length 819;
Best Local Similarity 26.4%; Pred. No. 3.7e+03;
RESULT 1231
ID AAB12755 standard; protein; 820 AA.
DE Streptococcus pneumoniae strain JNR7/87 BVH-11-2 protein antigen.
PN WO200039299-A2.
PD 06-JUL-2000.
PA (BIOC-) BIOCHEM PHARMA INC.
Query Match 11.8%; Score 54.5; DB 3; Length 820;
Best Local Similarity 26.4%; Pred. No. 3.7e+03;
RESULT 1232
ID AAY91939 standard; protein; 826 AA.
DE S. pneumoniae 92 kDa human C3-degrading protein.
PN WO200017370-A1.
PD 30-MAR-2000.
PA (MINU) UNIV MINNESOTA.
PA (AMCY) AMERICAN CYANAMID CO.
Query Match 11.8%; Score 54.5; DB 3; Length 826;
Best Local Similarity 26.4%; Pred. No. 3.7e+03;
RESULT 1233
ID AAY81662 standard; protein; 827 AA.
DE Streptococcus pneumoniae protein sequence ID311.
PN WO200006737-A2.
PD 10-FEB-2000.
PA (MICR-) MICROBIAL TECHNIQS LTD.
Query Match 11.8%; Score 54.5; DB 3; Length 827;
Best Local Similarity 26.4%; Pred. No. 3.7e+03;
RESULT 1234
ID AAB12759 standard; protein; 834 AA.
DE Streptococcus pneumoniae strain RX1 BVH-11-2 protein antigen.
PN WO200039299-A2.
PD 06-JUL-2000.
PA (BIOC-) BIOCHEM PHARMA INC.
Query Match 11.8%; Score 54.5; DB 3; Length 834;
Best Local Similarity 25.3%; Pred. No. 3.8e+03;
RESULT 1235
ID AAB12720 standard; protein; 838 AA.
DE Streptococcus pneumoniae BVH-11-2 protein antigen SEQ ID NO:14.
PN WO200039299-A2.
PD 06-JUL-2000.
PA (BIOC-) BIOCHEM PHARMA INC.
Query Match 11.8%; Score 54.5; DB 3; Length 838;
Best Local Similarity 26.4%; Pred. No. 3.8e+03;
RESULT 1236
ID AAB01466 standard; protein; 838 AA.
DE Recombinant variant of Sp36 (Sp36D) of S. pneumoniae.
PN WO200037105-A2.
PD 29-JUN-2000.
PA (MEDI-) MEDIMMUNE INC.
Query Match 11.8%; Score 54.5; DB 3; Length 838;
Best Local Similarity 26.4%; Pred. No. 3.8e+03;
RESULT 1237
ID AAU75934 standard; protein; 838 AA.
DE Streptococcus pneumoniae BVH-11-2 protein.
PN WO200198334-A2.
PD 27-DEC-2001.
PA (SHIR-) SHIRE BIOCHEM INC.
Query Match 11.8%; Score 54.5; DB 5; Length 838;
Best Local Similarity 26.4%; Pred. No. 3.8e+03;
RESULT 1238
ID ABM18798 standard; protein; 838 AA.
DE S. pneumoniae BVH-11-2 polypeptide SEQ ID NO: 9.
PN WO2003054007-A2.
PD 03-JUL-2003.

PA (SHIR-) SHIRE BIOCHEM INC.
Query Match 11.8%; Score 54.5; DB 7; Length 838;
Best Local Similarity 26.4%; Pred. No. 3.8e+03;
RESULT 1239
ID ADK48710 standard; protein; 838 AA.
DE Streptococcus pneumoniae protein, Seq ID NO 5225.
PN US6699703-B1.
PD 02-MAR-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 11.8%; Score 54.5; DB 8; Length 838;
Best Local Similarity 26.4%; Pred. No. 3.8e+03;
RESULT 1240
ID ABU01418 standard; protein; 839 AA.
DE S. pneumoniae type 4 strain protein from coding region #993.
PN WO200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 11.8%; Score 54.5; DB 6; Length 839;
Best Local Similarity 26.4%; Pred. No. 3.8e+03;
RESULT 1241
ID ADM2151 standard; protein; 839 AA.
DE S. pneumoniae antigenic protein sequence SeqID348.
PN WO2004020609-A2.
PD 11-MAR-2004.
PA (TUFT) UNIV TUFTS.
Query Match 11.8%; Score 54.5; DB 8; Length 839;
Best Local Similarity 26.4%; Pred. No. 3.8e+03;
RESULT 1242
ID AAY33920 standard; protein; 917 AA.
DE A Bcl-2 associated transcription factor called btf.
PN WO957535-A2.
PD 11-NOV-1999.
PA (RUTF) UNIV RUTGERS STATE NEW JERSEY.
Query Match 11.8%; Score 54.5; DB 3; Length 917;
Best Local Similarity 30.4%; Pred. No. 4.3e+03;
RESULT 1243
ID ADE58793 standard; protein; 921 AA.
DE Human Protein D79986, SEQ ID NO 4680.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 11.8%; Score 54.5; DB 7; Length 921;
Best Local Similarity 30.4%; Pred. No. 4.3e+03;
RESULT 1244
ID ABG16236 standard; protein; 930 AA.
DE Novel human diagnostic protein #16227.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.8%; Score 54.5; DB 4; Length 930;
Best Local Similarity 30.4%; Pred. No. 4.4e+03;
RESULT 1245
ID ABP65550 standard; protein; 1030 AA.
DE Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:294.
PN EP1227152-A1.
PD 31-JUL-2002.
PA (NEST) SOC PROD NESTLE SA.
Query Match 11.8%; Score 54.5; DB 5; Length 1030;
Best Local Similarity 30.4%; Pred. No. 5.1e+03;
RESULT 1246
ID ABG19044 standard; protein; 1058 AA.
DE Novel human diagnostic protein #19035.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.8%; Score 54.5; DB 4; Length 1058;
Best Local Similarity 23.3%; Pred. No. 5.3e+03;
RESULT 1247
ID ADA99480 standard; protein; 1290 AA.
DE Staphylococcus aureus antigenic protein #19.
PN WO2003011899-A2.

PD 13-FEB-2003.
PA (UYSH-) UNIV SHEFFIELD.
PA (BIOS-) BIOSYNEXUS INC.
Query Match 11.8%; Score 54.5; DB 6; Length 1290;
Best Local Similarity 24.7%; Pred. No. 6.9e+03;
RESULT 1248
ID ABP73292 standard; protein; 1373 AA.
DE Candida albicans essential protein SEQ ID NO 7129.
PN WO200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.8%; Score 54.5; DB 5; Length 1373;
Best Local Similarity 30.0%; Pred. No. 7.6e+03;
RESULT 1249
ID ABB71963 standard; protein; 1406 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 42681.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 11.8%; Score 54.5; DB 4; Length 1406;
Best Local Similarity 30.3%; Pred. No. 7.8e+03;
RESULT 1250
ID ABB65521 standard; protein; 1419 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 23355.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 11.8%; Score 54.5; DB 4; Length 1419;
Best Local Similarity 27.4%; Pred. No. 7.9e+03;
RESULT 1251
ID AAU71956 standard; protein; 1532 AA.
DE Human bone marrow tissue polypeptide #34.
PN WO200173447-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.8%; Score 54.5; DB 4; Length 1532;
Best Local Similarity 21.9%; Pred. No. 8.8e+03;
RESULT 1252
ID AAW54145 standard; protein; 1639 AA.
DE P. falciparum synthetic gp190 protein.
PN WO9814583-A2.
PD 09-APR-1998.
PA (BUJA/) BUJARD H.
Query Match 11.8%; Score 54.5; DB 2; Length 1639;
Best Local Similarity 31.6%; Pred. No. 9.7e+03;
RESULT 1253
ID AAE29345 standard; protein; 1639 AA.
DE Plasmodium falciparum merozoite surface protein-1 (MSP-1).
PN WO200270542-A2.
PD 12-SEP-2002.
PA (SELI-) ST ELIZABETH'S MEDICAL CENT INC.
Query Match 11.8%; Score 54.5; DB 5; Length 1639;
Best Local Similarity 31.6%; Pred. No. 9.7e+03;
RESULT 1254
ID AAP50777 standard; protein; 1654 AA.
DE Sequence of the P195 protein of Plasmodium falciparum.
PN EP154454-A.
PD 11-SEP-1985.
PA (WELL) WELLCOME FOUND LTD.
Query Match 11.8%; Score 54.5; DB 1; Length 1654;
Best Local Similarity 31.6%; Pred. No. 9.8e+03;
RESULT 1255
ID ABB63145 standard; protein; 1723 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 16227.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 11.8%; Score 54.5; DB 4; Length 1723;
Best Local Similarity 25.3%; Pred. No. 1e+04;
RESULT 1256
ID ABM68686 standard; protein; 1733 AA.
DE Photorhabdus luminescens protein sequence #1783.
PN WO200294867-A2.

PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 11.8%; Score 54.5; DB 6; Length 1733;
Best Local Similarity 28.8%; Pred. No. 1.1e+04;
RESULT 1257
ID ABR52606 standard; protein; 2000 AA.
DE Protein sequence #SEQ ID 77.
PD EPI258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match 11.8%; Score 54.5; DB 6; Length 2000;
Best Local Similarity 30.3%; Pred. No. 1.3e+04;
RESULT 1258
ID ADR63610 standard; protein; 2000 AA.
DE Disease treating protein complex-derived protein #848.
PD EPI338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 11.8%; Score 54.5; DB 7; Length 2072;
Best Local Similarity 30.3%; Pred. No. 1.3e+04;
RESULT 1259
ID ADI26354 standard; protein; 2072 AA.
DE Fusarium graminearum polyketide synthetase SEQ ID NO:6.
PD WO2004005522-A2.
PD 15-JAN-2004.
PA (BADI) BASF AG.
Query Match 11.8%; Score 54.5; DB 8; Length 2072;
Best Local Similarity 31.7%; Pred. No. 1.3e+04;
RESULT 1260
ID AAU37120 standard; protein; 2344 AA.
DE Staphylococcus aureus cellular proliferation protein #1290.
PD WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.8%; Score 54.5; DB 4; Length 2344;
Best Local Similarity 22.6%; Pred. No. 1.6e+04;
RESULT 1261
ID ABE58396 standard; protein; 2362 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 1980.
PD WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 11.8%; Score 54.5; DB 4; Length 2362;
Best Local Similarity 37.5%; Pred. No. 1.6e+04;
RESULT 1262
ID ABU42253 standard; protein; 3533 AA.
DE Protein encoded by Prokaryotic essential gene #27780.
PD WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.8%; Score 54.5; DB 6; Length 3533;
Best Local Similarity 24.7%; Pred. No. 2.8e+04;
RESULT 1263
ID AAU37403 standard; protein; 6281 AA.
DE Staphylococcus aureus cellular proliferation protein #1573.
PD WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.8%; Score 54.5; DB 4; Length 6281;
Best Local Similarity 24.7%; Pred. No. 6.3e+04;
RESULT 1264
ID ABU15887 standard; protein; 6713 AA.
DE Protein encoded by Prokaryotic essential gene #1414.
PD WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.8%; Score 54.5; DB 6; Length 6713;
Best Local Similarity 24.7%; Pred. No. 6.9e+04;
RESULT 1265
ID ABW73008 standard; protein; 9335 AA.
DE Staphylococcus aureus protein #2248.
PD WO200294868-A2.

PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 11.8%; Score 54.5; DB 6; Length 9535;
Best Local Similarity 24.7%; Pred. No. 1.1e+05;
RESULT 1266
ID ABJ19119 standard; protein; 10498 AA.
DE Pathogen specific antigen related staphylococcal protein SEQ ID No 440.
PD WO200259148-A2.
PD 01-AUG-2002.
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
Query Match 11.8%; Score 54.5; DB 6; Length 10498;
Best Local Similarity 24.7%; Pred. No. 1.3e+05;
RESULT 1267
ID AAM91782 standard; protein; 58 AA.
DE Human immune/haematopoietic antigen SEQ ID NO:19375.
PD WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.7%; Score 54; DB 4; Length 58;
Best Local Similarity 29.8%; Pred. No. 1e+02;
RESULT 1268
ID ABF34245 standard; protein; 74 AA.
DE Human ORF3218 protein, SEQ ID NO:6436.
PD WO200190366-A2.
PD 29-NOV-2001.
PA (CURA-) CURAGEN CORP.
Query Match 11.7%; Score 54; DB 5; Length 74;
Best Local Similarity 40.5%; Pred. No. 1.5e+02;
RESULT 1269
ID AAY41661 standard; protein; 75 AA.
DE Triticum aestivum XIAP associated factor 1 protein portion.
PD WO9947688-A1.
PD 23-SEP-1999.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 11.7%; Score 54; DB 2; Length 75;
Best Local Similarity 37.1%; Pred. No. 1.5e+02;
RESULT 1270
ID ABG18764 standard; protein; 99 AA.
DE Novel human diagnostic protein #18755.
PD WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.7%; Score 54; DB 4; Length 99;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
RESULT 1271
ID AAU50668 standard; protein; 106 AA.
DE Propionibacterium acnes immunogenic protein #11564.
PD WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 11.7%; Score 54; DB 4; Length 106;
Best Local Similarity 28.4%; Pred. No. 2.4e+02;
RESULT 1272
ID ARM47187 standard; protein; 106 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #11863.
PD WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 11.7%; Score 54; DB 6; Length 106;
Best Local Similarity 28.4%; Pred. No. 2.4e+02;
RESULT 1273
ID ABP63843 standard; protein; 111 AA.
DE Human ORF213.
PD US2002082206-A1.
PD 27-JUN-2002.
PA (LEAC/) LEACH M D.
PA (MEHR/) MEHRABAN F.
PA (CONL/) CONLEY P B.
PA (TOPP/) TOPPER J N.
PA (LAWD/) LAW D.
Query Match 11.7%; Score 54; DB 5; Length 111;
Best Local Similarity 24.1%; Pred. No. 2.6e+02;
RESULT 1274

ID AAB43352 standard; protein; 138 AA.
DE Human ORFX ORF3116 polypeptide sequence SEQ ID NO:6232.
PN WO2000058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 11.7%; Score 54; DB 3; Length 138;
Best Local Similarity 32.7%; Pred. No. 3.5e+02;
RESULT 1275
ID ABR08478 standard; protein; 138 AA.
DE Human ORFX protein sequence SEQ ID NO:16938.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match 11.7%; Score 54; DB 5; Length 138;
Best Local Similarity 32.7%; Pred. No. 3.5e+02;
RESULT 1276
ID ADC95852 standard; protein; 139 AA.
DE E. faecium protein sequence SEQ ID 5479.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 11.7%; Score 54; DB 7; Length 139;
Best Local Similarity 21.0%; Pred. No. 3.5e+02;
RESULT 1277
ID ADH86409 standard; protein; 143 AA.
DE Enterococcus faecalis polypeptide #889.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 11.7%; Score 54; DB 7; Length 143;
Best Local Similarity 39.4%; Pred. No. 3.7e+02;
RESULT 1278
ID AAR98944 standard; protein; 144 AA.
DE Humanised anti-CD38 monoclonal antibody heavy chain.
PN WO9616990-A1.
PD 06-JUN-1996.
PA (WELL) WELLCOME FOUND LTD.
Query Match 11.7%; Score 54; DB 2; Length 144;
Best Local Similarity 24.7%; Pred. No. 3.7e+02;
RESULT 1279
ID AAB32388 standard; protein; 154 AA.
DE Human secreted protein sequence encoded by gene 18 SEQ ID NO:74.
PN WO200047602-A1.
PD 17-AUG-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.7%; Score 54; DB 3; Length 154;
Best Local Similarity 23.2%; Pred. No. 4.1e+02;
RESULT 1280
ID ABP27245 standard; protein; 158 AA.
DE Streptococcus polypeptide SEQ ID NO 3666.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 11.7%; Score 54; DB 5; Length 158;
Best Local Similarity 25.8%; Pred. No. 4.2e+02;
RESULT 1281
ID ABR40625 standard; protein; 168 AA.
DE Oryza sativa oil trait related protein sequence SEQ ID NO:70.
PN WO2003002751-A2.
PD 09-JAN-2003.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 11.7%; Score 54; DB 6; Length 168;
Best Local Similarity 29.4%; Pred. No. 4.6e+02;
RESULT 1282
ID ADC23549 standard; protein; 168 AA.
DE Polypeptide involved in altering plant oil phenotype (SeqID 54).
PN WO2003001902-A2.
PD 09-JAN-2003.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.

Query Match 11.7%; Score 54; DB 7; Length 168;
Best Local Similarity 29.4%; Pred. No. 4.6e+02;
RESULT 1283
ID ABB68993 standard; protein; 185 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 33771.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 11.7%; Score 54; DB 4; Length 185;
Best Local Similarity 32.1%; Pred. No. 5.2e+02;
RESULT 1284
ID ADL67146 standard; protein; 188 AA.
DE Mouse B7-H6(5CD) protein SEQ ID NO:16.
PN WO2004022594-A2.
PD 18-MAR-2004.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
Query Match 11.7%; Score 54; DB 8; Length 188;
Best Local Similarity 27.0%; Pred. No. 5.4e+02;
RESULT 1285
ID ADL05642 standard; protein; 192 AA.
DE M. catarrhalis protein #1408.
PN US6673910-B1.
PD 06-JAN-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 11.7%; Score 54; DB 8; Length 192;
Best Local Similarity 22.4%; Pred. No. 5.5e+02;
RESULT 1286
ID ABR53514 standard; protein; 201 AA.
DE Protein sequence #SEQ ID 1893.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match 11.7%; Score 54; DB 6; Length 201;
Best Local Similarity 27.3%; Pred. No. 5.9e+02;
RESULT 1287
ID ADK64458 standard; protein; 201 AA.
DE Disease treating protein complex-derived protein #1146.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 11.7%; Score 54; DB 7; Length 201;
Best Local Similarity 27.3%; Pred. No. 5.9e+02;
RESULT 1288
ID AAG92761 standard; protein; 218 AA.
DE C. glutamicum protein fragment SEQ ID NO: 6515.
PN EP108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 11.7%; Score 54; DB 4; Length 218;
Best Local Similarity 27.8%; Pred. No. 6.6e+02;
RESULT 1289
ID ABU35298 standard; protein; 236 AA.
DE Protein encoded by Prokaryotic essential gene #20825.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.7%; Score 54; DB 6; Length 236;
Best Local Similarity 22.4%; Pred. No. 7.4e+02;
RESULT 1290
ID ABB63027 standard; protein; 245 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 15873.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 11.7%; Score 54; DB 4; Length 245;
Best Local Similarity 43.6%; Pred. No. 7.8e+02;
RESULT 1291
ID ADC79322 standard; protein; 262 AA.
DE Human G protein coupled receptor X (GPCRX) cDNA seq id 8.
PN US2003083463-A1.
PD 01-MAY-2003.
PA (PADI) PADIGARU M.
PA (KEKU) KEKUDA R.

PA (COLM/) COLMAN S D.
PA (SPYT/) SPYTEK K A.
PA (BALL/) BALLINGER R A.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (SHEN/) SHENOY S G.
PA (CASW/) CASMAN S J.
PA (GUSE/) GUSEV V Y.
Query Match 11.7%; Score 54; DB 7; Length 262;
Best Local Similarity 26.9%; Pred. No. 8.5e+02;
RESULT 1292
ID ADL67144 standard; protein; 280 AA.
DE Mouse B7-H6 protein SEQ ID NO:14.
PN WO2004022594-A2.
PD 18-MAR-2004.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
Query Match 11.7%; Score 54; DB 8; Length 280;
Best Local Similarity 27.0%; Pred. No. 9.4e+02;
RESULT 1293
ID ADN3513 standard; protein; 280 AA.
DE Murine STIGMA protein.
PN WO2004031105-A2.
PD 15-APR-2004.
PA (GRTH) GENENTECH INC.
Query Match 11.7%; Score 54; DB 8; Length 280;
Best Local Similarity 27.0%; Pred. No. 9.4e+02;
RESULT 1294
ID AAU61781 standard; protein; 295 AA.
DE Propionibacterium acnes immunogenic protein #22677.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 11.7%; Score 54; DB 4; Length 295;
Best Local Similarity 25.5%; Pred. No. 1e+03;
RESULT 1295
ID ABW58300 standard; protein; 295 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #22976.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 11.7%; Score 54; DB 6; Length 295;
Best Local Similarity 25.5%; Pred. No. 1e+03;
RESULT 1296
ID AAG45928 standard; protein; 309 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 57722.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 11.7%; Score 54; DB 3; Length 309;
Best Local Similarity 26.4%; Pred. No. 1.1e+03;
RESULT 1297
ID AAG09012 standard; protein; 309 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 6775.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 11.7%; Score 54; DB 3; Length 309;
Best Local Similarity 28.4%; Pred. No. 1.1e+03;
RESULT 1298
ID AAG45927 standard; protein; 315 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 57721.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 11.7%; Score 54; DB 3; Length 315;
Best Local Similarity 26.4%; Pred. No. 1.1e+03;
RESULT 1299
ID AAG09011 standard; protein; 315 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 6774.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 11.7%; Score 54; DB 3; Length 315;
Best Local Similarity 28.4%; Pred. No. 1.1e+03;
RESULT 1300
ID ABR40841 standard; protein; 317 AA.
DE Oryza sativa oil trait related protein sequence SEQ ID NO:465.
PN WO2003002751-A2.
PD 09-JAN-2003.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 11.7%; Score 54; DB 6; Length 317;
Best Local Similarity 29.4%; Pred. No. 1.1e+03;
RESULT 1301
ID ADC23680 standard; protein; 317 AA.
DE Polypeptide involved in altering plant oil phenotype (SeqID 212).
PN WO2003001902-A2.
PD 09-JAN-2003.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 11.7%; Score 54; DB 7; Length 317;
Best Local Similarity 29.4%; Pred. No. 1.1e+03;
RESULT 1302
ID ABM68098 standard; protein; 334 AA.
DE Photorhabdus luminescens protein sequence #1195.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 11.7%; Score 54; DB 6; Length 334;
Best Local Similarity 29.0%; Pred. No. 1.2e+03;
RESULT 1303
ID ADF05838 standard; protein; 338 AA.
DE Bacterial polypeptide #1951.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 11.7%; Score 54; DB 7; Length 338;
Best Local Similarity 35.8%; Pred. No. 1.2e+03;
RESULT 1304
ID ABU50042 standard; protein; 340 AA.
DE Protein encoded by Prokaryotic essential gene #35569.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.7%; Score 54; DB 6; Length 340;
Best Local Similarity 30.1%; Pred. No. 1.2e+03;
RESULT 1305
ID ABH57084 standard; protein; 367 AA.
DE Mouse ischaemic condition related protein sequence SEQ ID NO:184.
PN WO200188188-A2.
PD 22-NOV-2001.
PA (UVNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
Query Match 11.7%; Score 54; DB 5; Length 367;
Best Local Similarity 35.7%; Pred. No. 1.4e+03;
RESULT 1306
ID ABP78203 standard; protein; 369 AA.
DE N. gonorrhoeae amino acid sequence SEQ ID 2936.
PN WO200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Query Match 11.7%; Score 54; DB 6; Length 369;
Best Local Similarity 25.0%; Pred. No. 1.4e+03;
RESULT 1307
ID AAM93772 standard; protein; 376 AA.
DE Human polypeptide, SEQ ID NO: 3778.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 11.7%; Score 54; DB 4; Length 376;
Best Local Similarity 28.1%; Pred. No. 1.4e+03;
RESULT 1308
ID ABP69570 standard; protein; 376 AA.
DE Human polypeptide SEQ ID NO 1617.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 11.7%; Score 54; DB 5; Length 376;
Best Local Similarity 28.1%; Pred. No. 1.4e+03;
RESULT 1309

ID ABR47605 standard; protein; 376 AA.
DE Breast cancer associated protein sequence SEQ ID NO:451.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 11.7%; Score 54; DB 6; Length 376;
Best Local Similarity 28.1%; Pred. No. 1.4e+03;
RESULT 1310
ID ADL31745 standard; protein; 376 AA.
DE Human protein encoded by a full length cDNA clone SeqID 3778.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 11.7%; Score 54; DB 8; Length 376;
Best Local Similarity 28.1%; Pred. No. 1.4e+03;
RESULT 1311
ID ADO31117 standard; protein; 376 AA.
DE N-end rule ubiquitylation detection method protein #3.
PN WO2004042352-A2.
PD 21-MAY-2004.
PA (MESO-) MESO SCALE TECHNOLOGIES LLC.
Query Match 11.7%; Score 54; DB 8; Length 376;
Best Local Similarity 28.1%; Pred. No. 1.4e+03;
RESULT 1312
ID ABP81273 standard; protein; 397 AA.
DE Arabidopsis thaliana protein #101 modulated by PTGS.
PN WO200281695-A2.
PD 17-OCT-2002.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 11.7%; Score 54; DB 6; Length 397;
Best Local Similarity 26.4%; Pred. No. 1.5e+03;
RESULT 1313
ID ABH11731 standard; peptide; 415 AA.
DE Human granophilin-a homologue, SEQ ID NO:2101.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.7%; Score 54; DB 4; Length 415;
Best Local Similarity 28.1%; Pred. No. 1.6e+03;
RESULT 1314
ID ABB57755 standard; protein; 417 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 57.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 11.7%; Score 54; DB 4; Length 417;
Best Local Similarity 26.0%; Pred. No. 1.6e+03;
RESULT 1315
ID ABP57973 standard; protein; 428 AA.
DE Ferric-siderophore receptor FpA d2 domain 3.
PN WO200283843-A2.
PD 24-OCT-2002.
PA (DSQU-) D-SQUARED BIOTECHNOLOGIES INC.
Query Match 11.7%; Score 54; DB 6; Length 428;
Best Local Similarity 22.5%; Pred. No. 1.7e+03;
RESULT 1316
ID ABR38876 standard; protein; 428 AA.
DE Surface exposed immunogenic polypeptide (SEIP) # SEQ ID 2.
PN WO2003006672-A2.
PD 23-JAN-2003.
PA (DSQU-) D-SQUARED BIOTECHNOLOGIES INC.
Query Match 11.7%; Score 54; DB 6; Length 428;
Best Local Similarity 22.5%; Pred. No. 1.7e+03;
RESULT 1317
ID AAW05761 standard; protein; 430 AA.
DE Presenilin-1-2 D253A delta254-286 mutation.
PN WO9634099-A2.
PD 31-OCT-1996.
PA (HSCR-) HSC RES & DEV LP.
Query Match 11.7%; Score 54; DB 2; Length 430;
Best Local Similarity 21.0%; Pred. No. 1.7e+03;

RESULT 1318
ID AAW05760 standard; protein; 434 AA.
DE Presenilin-1-1 D257A delta258-290 mutation.
PN WO9634099-A2.
PD 31-OCT-1996.
PA (HSCR-) HSC RES & DEV LP.
Query Match 11.7%; Score 54; DB 2; Length 434;
Best Local Similarity 21.0%; Pred. No. 1.7e+03;
RESULT 1319
ID AAG53133 standard; protein; 465 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 67618.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 11.7%; Score 54; DB 3; Length 465;
Best Local Similarity 32.8%; Pred. No. 1.9e+03;
RESULT 1320
ID ABR52953 standard; protein; 481 AA.
DE Protein sequence #SEQ ID 771.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match 11.7%; Score 54; DB 6; Length 481;
Best Local Similarity 42.2%; Pred. No. 2e+03;
RESULT 1321
ID ADK62620 standard; protein; 481 AA.
DE Disease treating protein complex-derived protein #436.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 11.7%; Score 54; DB 7; Length 481;
Best Local Similarity 42.2%; Pred. No. 2e+03;
RESULT 1322
ID ABB60980 standard; protein; 494 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 9732.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 11.7%; Score 54; DB 4; Length 494;
Best Local Similarity 25.7%; Pred. No. 2.1e+03;
RESULT 1323
ID ABR47603 standard; protein; 501 AA.
DE Breast cancer associated protein sequence SEQ ID NO:447.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 11.7%; Score 54; DB 6; Length 501;
Best Local Similarity 28.1%; Pred. No. 2.1e+03;
RESULT 1324
ID RAP70320 standard; protein; 524 AA.
DE Protein G encoded by the entire sequence of the non-segmented negative
DE strand RNA of the rabies virus.
PN EP237686-A.
PD 23-SEP-1987.
PA (INSP) INST PASTEUR.
Query Match 11.7%; Score 54; DB 1; Length 524;
Best Local Similarity 26.6%; Pred. No. 2.3e+03;
RESULT 1325
ID ABU19782 standard; protein; 530 AA.
DE Protein encoded by Prokaryotic essential gene #5309.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.7%; Score 54; DB 6; Length 530;
Best Local Similarity 28.8%; Pred. No. 2.3e+03;
RESULT 1326
ID ABJ04826 standard; protein; 606 AA.
DE Avian hepatitis E virus ORF2 protein.
PN WO200253712-A2.
PD 11-JUL-2002.
PA (VIRG) VIRGINIA TECH INTELLECTUAL PROPERTIES.
Query Match 11.7%; Score 54; DB 5; Length 606;

Best Local Similarity 32.9%; Pred. No. 2.8e+03;
RESULT 1327
ID ADF04709 standard; protein; 606 AA.
DE Sea squirt protein with tissue specific expression in development Seq304.
FN JP2004057129-A.
PD 26-FEB-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 11.7%; Score 54; DB 8; Length 606;
Best Local Similarity 32.5%; Pred. No. 2.8e+03;
RESULT 1328
ID AAR25246 standard; protein; 608 AA.
DE Chicken Growth Hormone receptor.
FN EP492179-A2.
PD 01-JUL-1992.
PA (AWCY) AMERICAN CYANAMID CO.
Query Match 11.7%; Score 54; DB 2; Length 608;
Best Local Similarity 26.7%; Pred. No. 2.8e+03;
RESULT 1329
ID AAW68206 standard; protein; 610 AA.
DE M. catarrhalis strain TTA24 UspA2 antigen.
FN WO9828333-A2.
PD 02-JUL-1998.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 11.7%; Score 54; DB 2; Length 610;
Best Local Similarity 23.9%; Pred. No. 2.8e+03;
RESULT 1330
ID ABG17654 standard; protein; 639 AA.
DE Novel human diagnostic protein #17645.
FN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.7%; Score 54; DB 4; Length 639;
Best Local Similarity 24.1%; Pred. No. 3e+03;
RESULT 1331
ID AAB10934 standard; protein; 654 AA.
DE C. elegans rrm3p protein fragment.
FN WO200055316-A1.
PD 21-SEP-2000.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
Query Match 11.7%; Score 54; DB 3; Length 654;
Best Local Similarity 37.1%; Pred. No. 3.1e+03;
RESULT 1332
ID ABB48089 standard; protein; 664 AA.
DE Listeria monocytogenes protein #793.
FN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 11.7%; Score 54; DB 5; Length 664;
Best Local Similarity 27.4%; Pred. No. 3.2e+03;
RESULT 1333
ID ABU32728 standard; protein; 664 AA.
DE Protein encoded by Prokaryotic essential gene #18255.
FN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.7%; Score 54; DB 6; Length 664;
Best Local Similarity 27.4%; Pred. No. 3.2e+03;
RESULT 1334
ID ABG95647 standard; protein; 676 AA.
DE Human nucleic acid associated protein, NAAFP4, Incyte 2686104CD1.
FN WO200274913-A2.
PD 26-SEP-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 11.7%; Score 54; DB 5; Length 676;
Best Local Similarity 25.0%; Pred. No. 3.2e+03;
RESULT 1335
ID ADA54808 standard; protein; 676 AA.
DE Human protein, SEQ ID 2376.
FN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 11.7%; Score 54; DB 6; Length 676;

Best Local Similarity 25.0%; Pred. No. 3.2e+03;
RESULT 1336
ID ADI70692 standard; protein; 676 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID2498.
FN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 11.7%; Score 54; DB 7; Length 676;
Best Local Similarity 25.0%; Pred. No. 3.2e+03;
RESULT 1337
ID ABR41414 standard; protein; 680 AA.
DE Human D1THP zinc finger transcriptional regulator.
FN WO200297031-A2.
PD 05-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 11.7%; Score 54; DB 6; Length 680;
Best Local Similarity 25.0%; Pred. No. 3.3e+03;
RESULT 1338
ID ABB07847 standard; protein; 681 AA.
DE C. elegans protein identified by EMBL Accession No. AF000363.
FN WO200220747-A2.
PD 14-MAR-2002.
PA (FARB) BAYER AG.
Query Match 11.7%; Score 54; DB 5; Length 681;
Best Local Similarity 28.1%; Pred. No. 3.3e+03;
RESULT 1339
ID ABU29287 standard; protein; 685 AA.
DE Protein encoded by Prokaryotic essential gene #14814.
FN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.7%; Score 54; DB 6; Length 685;
Best Local Similarity 39.4%; Pred. No. 3.3e+03;
RESULT 1340
ID ADI60261 standard; protein; 705 AA.
DE Secreted polypeptide #145.
FN WO2003025142-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 11.7%; Score 54; DB 7; Length 705;
Best Local Similarity 25.0%; Pred. No. 3.4e+03;
RESULT 1341
ID AAR07077 standard; protein; 707 AA.
DE 92-kDa human type IV collagenase gene product.
FN EP398859-A.
PD 22-NOV-1990.
PA (UNIW) UNIV WASHINGTON.
Query Match 11.7%; Score 54; DB 2; Length 707;
Best Local Similarity 27.6%; Pred. No. 3.4e+03;
RESULT 1342
ID AAY58015 standard; protein; 707 AA.
DE Matrix metalloproteinase-9 (MMP-9) amino acid sequence.
FN WO9957315-A2.
PD 11-NOV-1999.
PA (ISIS-) ISIS INNOVATION LTD.
Query Match 11.7%; Score 54; DB 3; Length 707;
Best Local Similarity 27.6%; Pred. No. 3.4e+03;
RESULT 1343
ID AAB84611 standard; protein; 707 AA.
DE Amino acid sequence of matrix metalloproteinase-9.
FN WO200149309-A2.
PD 12-JUL-2001.
PA (PFIZ) PFIZER LTD.
PA (PFIZ) PFIZER INC.
Query Match 11.7%; Score 54; DB 4; Length 707;
Best Local Similarity 27.6%; Pred. No. 3.4e+03;
RESULT 1344
ID AAE10432 standard; protein; 707 AA.
DE Human matrix metalloproteinase-9 (MMP-9) protein.
FN WO200166766-A2.
PD 13-SEP-2001.
PA (DARW-) DARWIN MOLECULAR CORP.

PA (SCHA/) SCHATZMAN R.
 Query Match 11.7%; Score 54; DB 4; Length 707;
 Best Local Similarity 27.6%; Pred. No. 3.4e+03;
 RESULT 1345
 ID AAB20491 standard; protein; 707 AA.
 DE Human matrix metalloproteinase-9 (MMP-9).
 PN WO200126671-A1.
 PD 19-APR-2001.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 Query Match 11.7%; Score 54; DB 4; Length 707;
 Best Local Similarity 27.6%; Pred. No. 3.4e+03;
 RESULT 1346
 ID ABU56680 standard; protein; 707 AA.
 DE Lung cancer-associated polypeptide #273.
 PN WO200286443-A2.
 PD 31-OCT-2002.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Query Match 11.7%; Score 54; DB 6; Length 707;
 Best Local Similarity 27.6%; Pred. No. 3.4e+03;
 RESULT 1347
 ID ASU56467 standard; protein; 707 AA.
 DE Lung cancer-associated polypeptide #60.
 PN WO200286443-A2.
 PD 31-OCT-2002.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Query Match 11.7%; Score 54; DB 6; Length 707;
 Best Local Similarity 27.6%; Pred. No. 3.4e+03;
 RESULT 1348
 ID AAO16609 standard; protein; 707 AA.
 DE Human matrix metalloproteinase 9 (MMP9) gelatinase protein.
 PN WO2003002729-A1.
 PD 09-JAN-2003.
 PA (ASTR) ASTRAZENECA AB.
 Query Match 11.7%; Score 54; DB 6; Length 707;
 Best Local Similarity 27.6%; Pred. No. 3.4e+03;
 RESULT 1349
 ID ABR92116 standard; protein; 707 AA.
 DE Human cervical cancer cell marker protein SEQ ID NO:142.
 PN WO2002101075-A2.
 PD 19-DEC-2002.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 11.7%; Score 54; DB 6; Length 707;
 Best Local Similarity 27.6%; Pred. No. 3.4e+03;
 RESULT 1350
 ID ADL14993 standard; protein; 707 AA.
 DE Human type IV collagenase protein for cancer treatment.
 PN WO2003068268-A2.
 PD 21-AUG-2003.
 PA (BIOI-) BIOINVENT INT AB.
 Query Match 11.7%; Score 54; DB 7; Length 707;
 Best Local Similarity 27.6%; Pred. No. 3.4e+03;
 RESULT 1351
 ID ADN39040 standard; protein; 707 AA.
 DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:358.
 PN WO2003042661-A2.
 PD 22-MAY-2003.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Query Match 11.7%; Score 54; DB 7; Length 707;
 Best Local Similarity 27.6%; Pred. No. 3.4e+03;
 RESULT 1352
 ID ADN39935 standard; protein; 707 AA.
 DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C305.
 PN WO2003042661-A2.
 PD 22-MAY-2003.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Query Match 11.7%; Score 54; DB 7; Length 707;
 Best Local Similarity 27.6%; Pred. No. 3.4e+03;
 RESULT 1353
 ID ADH17067 standard; protein; 707 AA.
 DE Human matrix metalloproteinase 9 (MMP9) protein.
 PN WO2003097854-A2.
 PD 27-NOV-2003.

PA (SUGE-) SUGEN INC.
 Query Match 11.7%; Score 54; DB 8; Length 707;
 Best Local Similarity 27.6%; Pred. No. 3.4e+03;
 RESULT 1354
 ID ADJ75581 standard; protein; 707 AA.
 DE Marker gene related amino acid sequence SEQ ID NO:833.
 PN EPI394274-A2.
 PD 03-MAR-2004.
 PA (GENO-) GENOX RES INC.
 Query Match 11.7%; Score 54; DB 8; Length 707;
 Best Local Similarity 27.6%; Pred. No. 3.4e+03;
 RESULT 1355
 ID ADM67186 standard; protein; 707 AA.
 DE Human adipocyte specific matrix metalloproteinase 9 protein SeqID 539.
 PN WO2004011618-A2.
 PD 05-FEB-2004.
 PA (HMGE-) HMGNE INC.
 Query Match 11.7%; Score 54; DB 8; Length 707;
 Best Local Similarity 27.6%; Pred. No. 3.4e+03;
 RESULT 1356
 ID ADN07701 standard; protein; 707 AA.
 DE Human matrix metalloproteinase 9 protein.
 PN US2004071687-A1.
 PD 15-APR-2004.
 PA (RAFI/) RAFII S.
 PA (HEIS/) HEISSIG B.
 PA (HATT/) HATTORI K.
 Query Match 11.7%; Score 54; DB 8; Length 707;
 Best Local Similarity 27.6%; Pred. No. 3.4e+03;
 RESULT 1357
 ID ADQ19168 standard; protein; 707 AA.
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1987.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 11.7%; Score 54; DB 8; Length 707;
 Best Local Similarity 27.6%; Pred. No. 3.4e+03;
 RESULT 1358
 ID ABU25591 standard; protein; 739 AA.
 DE Protein encoded by Prokaryotic essential gene #11118.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 11.7%; Score 54; DB 6; Length 739;
 Best Local Similarity 29.3%; Pred. No. 3.7e+03;
 RESULT 1359
 ID ABM65407 standard; protein; 767 AA.
 DE Propionibacterium acnes immunogenic polypeptide #30083.
 PN WO2003033515-A1.
 PD 24-APR-2003.
 PA (CORI-) CORIXA CORP.
 Query Match 11.7%; Score 54; DB 6; Length 767;
 Best Local Similarity 28.6%; Pred. No. 3.9e+03;
 RESULT 1360
 ID AAU67605 standard; protein; 775 AA.
 DE Propionibacterium acnes immunogenic protein #28501.
 PN WO200181581-A2.
 PD 01-NOV-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 11.7%; Score 54; DB 4; Length 775;
 Best Local Similarity 28.6%; Pred. No. 3.9e+03;
 RESULT 1361
 ID ABM64124 standard; protein; 775 AA.
 DE Propionibacterium acnes predicted ORF-encoded polypeptide #28800.
 PN WO2003033515-A1.
 PD 24-APR-2003.
 PA (CORI-) CORIXA CORP.
 Query Match 11.7%; Score 54; DB 6; Length 775;
 Best Local Similarity 28.6%; Pred. No. 3.9e+03;
 RESULT 1362
 ID ABG11008 standard; protein; 791 AA.
 DE Novel human diagnostic protein #10999.
 PN WO200175067-A2.

PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC. 11.7%; Score 54; DB 4; Length 791;
Query Match 45.5%; Pred. No. 4e+03;
Best Local Similarity 45.5%; Pred. No. 4e+03;
RESULT 1363
ID ABG05452 standard; protein; 791 AA.
DE Novel human diagnostic protein #5443.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC. 11.7%; Score 54; DB 4; Length 791;
Query Match 45.5%; Pred. No. 4e+03;
Best Local Similarity 45.5%; Pred. No. 4e+03;
RESULT 1364
ID ABG28157 standard; protein; 834 AA.
DE Novel human diagnostic protein #28148.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC. 11.7%; Score 54; DB 4; Length 834;
Query Match 24.6%; Pred. No. 4.3e+03;
Best Local Similarity 24.6%; Pred. No. 4.3e+03;
RESULT 1365
ID AAW56309 standard; protein; 854 AA.
DE Clas II S-receptor kinase (SRK) amino acid sequence.
PN JP10099076-A.
PD 21-APR-1998.
PA (SAIS-) SAISHU JITSUYO GIJUTSU KENKYUSHO KK.
Query Match 11.7%; Score 54; DB 2; Length 854;
Best Local Similarity 25.8%; Pred. No. 4.5e+03;
RESULT 1366
ID ADA34240 standard; protein; 862 AA.
DE Acinetobacter baumannii protein #1401.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 11.7%; Score 54; DB 6; Length 862;
Best Local Similarity 34.1%; Pred. No. 4.5e+03;
RESULT 1367
ID ABB6483 standard; protein; 865 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 20241.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY. 11.7%; Score 54; DB 4; Length 865;
Query Match 28.0%; Pred. No. 4.6e+03;
Best Local Similarity 28.0%; Pred. No. 4.6e+03;
RESULT 1368
ID AAU15071 standard; protein; 871 AA.
DE Protein encoded by C. albicans essential gene CayHR172W (SPC97).
PN WO200160975-A2.
PD 23-AUG-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.7%; Score 54; DB 4; Length 871;
Best Local Similarity 27.9%; Pred. No. 4.6e+03;
RESULT 1369
ID ABP73213 standard; protein; 871 AA.
DE Candida albicans essential protein SEQ ID NO 7050.
PN WO200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.7%; Score 54; DB 5; Length 871;
Best Local Similarity 27.9%; Pred. No. 4.6e+03;
RESULT 1370
ID ABG37578 standard; protein; 908 AA.
DE RTX-like protein encoded by E. coli CFT073 ORF5.
PN WO200259320-A2.
PD 01-AUG-2002.
PA (WISC) WISCONSIN ALUMNI RES FOUND.
Query Match 11.7%; Score 54; DB 5; Length 908;
Best Local Similarity 30.7%; Pred. No. 4.9e+03;
RESULT 1371
ID ADH80655 standard; protein; 908 AA.
DE Escherichia coli CFT073 genome contig associated protein #3.
PN US2003165870-A1.
PD 04-SEP-2003.

PA (BLAT/) BLATTNER F R. 11.7%; Score 54; DB 7; Length 908;
PA (WELC/) WELCH R A.
PA (BURL/) BURLAND V D.
Query Match 30.7%; Pred. No. 4.9e+03;
Best Local Similarity 30.7%; Pred. No. 4.9e+03;
RESULT 1372
ID ABO84013 standard; protein; 922 AA.
DE Pseudomonas aeruginosa polypeptide #16188.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 11.7%; Score 54; DB 7; Length 922;
Best Local Similarity 29.3%; Pred. No. 5e+03;
RESULT 1373
ID ADJ50989 standard; protein; 951 AA.
DE Human novel protein NOV21a.
PN US2004030096-A1.
PD 12-FEB-2004.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (EDIN/) EDINGER S R.
PA (PADI/) PADIGARU M.
PA (GUOX/) GUO X.
PA (KEKU/) KEKUDA R.
PA (ZHON/) ZHONG M.
PA (PATT/) PATTURAJAN M.
PA (MILL/) MILLER C E.
PA (JTWV/) JI W.
PA (PENA/) PENA C E A.
PA (BURG/) BURGESS C E.
PA (SCIO/) SCIORE P.
PA (STON/) STONE D J.
PA (TAUP/) TAUPIER R J.
PA (CASW/) CASMAN S J.
PA (ROTH/) ROTHENBERG M E.
PA (MALY/) MALYANKAR U M.
PA (BOLD/) BOLDOG F L.
Query Match 11.7%; Score 54; DB 8; Length 951;
Best Local Similarity 28.1%; Pred. No. 5.2e+03;
RESULT 1374
ID AAP81773 standard; protein; 1027 AA.
DE Sequence encoded by open reading frame of cDNA corresponding to HIV-2 ROD genome.
PN WO805440-A.
PD 28-JUL-1988.
PA (INSP) INST PASTEUR.
PA (ALIZ/) ALIZON M.
PA (CNRS) CENT NAT RECH SCI.
Query Match 11.7%; Score 54; DB 1; Length 1027;
Best Local Similarity 24.5%; Pred. No. 5.8e+03;
RESULT 1375
ID ADN74537 standard; protein; 1058 AA.
DE Thale cress protein repressed in E2Fa/Dpa expressing plants SeqID 2432.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDESIGN NV.
Query Match 11.7%; Score 54; DB 8; Length 1058;
Best Local Similarity 31.2%; Pred. No. 6.1e+03;
RESULT 1376
ID ADQ08600 standard; protein; 1067 AA.
DE Ciona intestinalis nervous system associated protein SeqID2.
PN JP2004057127-A.
PD 26-FEB-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 11.7%; Score 54; DB 8; Length 1067;
Best Local Similarity 29.5%; Pred. No. 6.1e+03;
RESULT 1377
ID ABB69366 standard; protein; 1068 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 34890.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY. 11.7%; Score 54; DB 4; Length 1068;
Query Match

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Best Local Similarity 29.0%; Pred. No. 6.1e+03;
RESULT 1378
ID ABG29358 standard; protein; 1102 AA.
DE Novel human diagnostic protein #29349.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.7%; Score 54; DB 4; Length 1102;
Best Local Similarity 28.1%; Pred. No. 6.4e+03;
RESULT 1379
ID ADJ57489 standard; protein; 1102 AA.
DE Human polypeptide.
PN WO2004006753-A2.
PD 22-JAN-2004.
PA (SEAT-) SEATTLE GENETICS INC.
Query Match 11.7%; Score 54; DB 8; Length 1102;
Best Local Similarity 28.1%; Pred. No. 6.4e+03;
RESULT 1380
ID ABU32051 standard; protein; 1137 AA.
DE Protein encoded by Prokaryotic essential gene #17578.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.7%; Score 54; DB 6; Length 1137;
Best Local Similarity 21.6%; Pred. No. 6.7e+03;
RESULT 1381
ID AB067057 standard; protein; 1138 AA.
DE Klebsiella pneumoniae polypeptide seqid 13574.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 11.7%; Score 54; DB 7; Length 1138;
Best Local Similarity 21.6%; Pred. No. 6.7e+03;
RESULT 1382
ID ABG14968 standard; protein; 1182 AA.
DE Novel human diagnostic protein #14959.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.7%; Score 54; DB 4; Length 1182;
Best Local Similarity 24.0%; Pred. No. 7.1e+03;
RESULT 1383
ID ABU33690 standard; protein; 1265 AA.
DE Protein encoded by Prokaryotic essential gene #19217.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.7%; Score 54; DB 6; Length 1265;
Best Local Similarity 27.2%; Pred. No. 7.8e+03;
RESULT 1384
ID ABG25490 standard; protein; 1302 AA.
DE Novel human diagnostic protein #25481.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.7%; Score 54; DB 4; Length 1302;
Best Local Similarity 24.0%; Pred. No. 8.1e+03;
RESULT 1385
ID ABG29625 standard; protein; 1393 AA.
DE Novel human diagnostic protein #29616.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.7%; Score 54; DB 4; Length 1393;
Best Local Similarity 24.0%; Pred. No. 8.9e+03;
RESULT 1386
ID ABB52738 standard; protein; 1684 AA.
DE Escherichia coli polypeptide SEQ ID NO 877.
PN WO200166572-A2.
PD 13-SEP-2001.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
Query Match 11.7%; Score 54; DB 4; Length 1684;
Best Local Similarity 30.7%; Pred. No. 1.2e+04;

Best Local Similarity 11.7%; Score 54; DB 4; Length 1963;
RESULT 1387
ID ABB62819 standard; protein; 1963 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 15249.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 11.7%; Score 54; DB 4; Length 1963;
Best Local Similarity 28.3%; Pred. No. 1.4e+04;
RESULT 1388
ID ABB64823 standard; protein; 2119 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 21261.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 11.7%; Score 54; DB 4; Length 2119;
Best Local Similarity 37.1%; Pred. No. 1.6e+04;
RESULT 1389
ID AAR52580 standard; protein; 2308 AA.
DE RPTP-beta amino acid sequence.
PN WO9409037-A1.
PD 28-APR-1994.
PA (UINY-) UNIV NEW YORK MEDICAL CENT.
Query Match 11.7%; Score 54; DB 2; Length 2308;
Best Local Similarity 24.7%; Pred. No. 1.8e+04;
RESULT 1390
ID ABB62231 standard; protein; 2441 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 13485.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 11.7%; Score 54; DB 4; Length 2441;
Best Local Similarity 28.3%; Pred. No. 1.9e+04;
RESULT 1391
ID ABU61813 standard; protein; 2462 AA.
DE Mouse nuclear receptor corepressor SMRTE.
PN US2003027137-A1.
PD 06-FEB-2003.
PA (CHEN/) CHEN J D.
Query Match 11.7%; Score 54; DB 6; Length 2462;
Best Local Similarity 22.9%; Pred. No. 2e+04;
RESULT 1392
ID ABU12083 standard; protein; 2572 AA.
DE Human NOV25b CG93858-02 protein SEQ ID 86.
PN WO200281625-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 11.7%; Score 54; DB 6; Length 2572;
Best Local Similarity 25.6%; Pred. No. 2.1e+04;
RESULT 1393
ID ADK60225 standard; protein; 2673 AA.
DE Angiogenesis differentially expressed protein GS-P52.
PN FR2836687-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 11.7%; Score 54; DB 8; Length 2673;
Best Local Similarity 25.6%; Pred. No. 2.2e+04;
RESULT 1394
ID ADK60526 standard; protein; 2673 AA.
DE Angiogenesis differentially expressed protein GS-P52.
PN FR2836686-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 11.7%; Score 54; DB 8; Length 2673;
Best Local Similarity 25.6%; Pred. No. 2.2e+04;
RESULT 1395
ID ADP73149 standard; protein; 2673 AA.
DE Angiogenesis inhibitor human protein sequence, GS-P52.
PN FR2843753-A1.
PD 27-FEB-2004.
PA (GENE/) GENE S.
PA (ALMS/) AL M S.
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Query Match
 Best Local Similarity 11.7%; Score 54; DB 8; Length 2673;
 RESULT 1396
 ID ADJ83136 standard; protein; 3645 AA.
 DE Human hemocentrin protein - SEQ ID 127.
 PN US2003170630-A1.
 PD 11-SEP-2003.
 PA (ALSO/) ALSOROOK J P.
 PA (TCHE/) TCHERNEV V T.
 PA (LIUX/) LIU X.
 PA (SPYT/) SPYTEK K A.
 PA (ZERH/) ZERHUSEN B D.
 PA (PATT/) PATTURAJAN M.
 PA (LEPL/) LEPLEY D M.
 PA (BURG/) BURGESS C E.
 PA (SHIM/) SHIMKETS R A.
 PA (GROS/) GROSSE W M.
 PA (SZEK/) SZKERES E S.
 PA (VERN/) VERNET C A M.
 PA (LILL/) LI L.
 PA (CASM/) CASMAN S J.
 PA (BOLD/) BOLDOG F L.
 PA (GORM/) GORMAN L.
 PA (GANG/) GANGOLLI E A.
 PA (FERN/) FERNANDES E R.
 PA (RIEG/) RIEGER D K.
 PA (EDIN/) EDINGER S R.
 PA (GUNT/) GUNTHER E.
 PA (MILL/) MILLET I.
 PA (SCIO/) SCIORE P.
 PA (ELLE/) ELLERMAN K.
 PA (MACD/) MACDOUGALL J R.
 PA (SMIT/) SMITHSON G.
 Query Match
 Best Local Similarity 11.7%; Score 54; DB 7; Length 3645;
 RESULT 1397
 ID ABU69135 standard; protein; 4495 AA.
 DE Human NOVX polypeptide #10.
 PN WO200290504-A2.
 PD 14-NOV-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match
 Best Local Similarity 11.7%; Score 54; DB 6; Length 4495;
 RESULT 1398
 ID ADH72106 standard; protein; 4495 AA.
 DE Human protein of the invention NOV43c SEQ ID NO:1002.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match
 Best Local Similarity 11.7%; Score 54; DB 8; Length 4495;
 RESULT 1399
 ID ADO08273 standard; protein; 4495 AA.
 DE Human NOVX polypeptide #10.
 PN US2004018594-A1.
 PD 29-JAN-2004.
 PA (ALSO/) ALSOROOK J P.
 PA (ANDE/) ANDERSON D W.
 PA (BOLD/) BOLDOG F L.
 PA (BURG/) BURGESS C E.
 PA (CASM/) CASMAN S J.
 PA (CHAP/) CHAPOVAL A.
 PA (EDIN/) EDINGER S R.
 PA (GERL/) GERLACH V.
 PA (GORM/) GORMAN L.
 PA (GUNT/) GUNTHER E.
 PA (GUOX/) GUO X S.
 PA (KEKU/) KEKUDA R.
 PA (LEPL/) LEPLEY D M.
 PA (LILL/) LI L.
 PA (LIUX/) LIU X.
 PA (MALY/) MALLYANKAR U M.
 PA (MILL/) MILLER C B.

PA (MILL/) MILLET I.
 PA (PADI/) PADIGARU M.
 PA (PATT/) PATTURAJAN M.
 PA (PENA/) PENA C E A.
 PA (RIEG/) RIEGER D K.
 PA (SHEN/) SHENOY S G.
 PA (SHIM/) SHIMKETS R A.
 PA (SPYT/) SPYTEK K A.
 PA (TAUP/) TAUPIER R J.
 PA (VERN/) VERNET C A M.
 PA (VOSS/) VOSS E Z.
 PA (ZERH/) ZERHUSEN B D.
 Query Match
 Best Local Similarity 11.7%; Score 54; DB 8; Length 4495;
 RESULT 1400
 ID ABF60991 standard; protein; 5635 AA.
 DE Novel human protein. SEQ ID 78.
 PN WO200250105-A1.
 PD 27-JUN-2002.
 PA (SMIK/) SMITHKLINE BEECHAM CORP.
 PA (SMIK/) SMITHKLINE BEECHAM PLC.
 PA (GLAX/) GLAXO GROUP LTD.
 Query Match
 Best Local Similarity 11.7%; Score 54; DB 5; Length 5635;
 RESULT 1401
 ID ADJ70089 standard; protein; 5636 AA.
 DE Human heat mitochondrial protein as a therapeutic target SeqID1895.
 PN WO2003087768-A2.
 PD 23-OCT-2003.
 PA (MITO-) MITOKOR.
 PA (BUCK-) BUCK INST AGE RES.
 Query Match
 Best Local Similarity 11.7%; Score 54; DB 7; Length 5636;
 RESULT 1402
 ID ADH83137 standard; protein; 5636 AA.
 DE Human hemocentrin protein - SEQ ID 128.
 PN US2003170630-A1.
 PD 11-SEP-2003.
 PA (ALSO/) ALSOROOK J P.
 PA (TCHE/) TCHERNEV V T.
 PA (LIUX/) LIU X.
 PA (SPYT/) SPYTEK K A.
 PA (ZERH/) ZERHUSEN B D.
 PA (PATT/) PATTURAJAN M.
 PA (LEPL/) LEPLEY D M.
 PA (BURG/) BURGESS C E.
 PA (SHIM/) SHIMKETS R A.
 PA (GROS/) GROSSE W M.
 PA (SZEK/) SZKERES E S.
 PA (VERN/) VERNET C A M.
 PA (LILL/) LI L.
 PA (CASM/) CASMAN S J.
 PA (BOLD/) BOLDOG F L.
 PA (GORM/) GORMAN L.
 PA (GANG/) GANGOLLI E A.
 PA (FERN/) FERNANDES E R.
 PA (RIEG/) RIEGER D K.
 PA (EDIN/) EDINGER S R.
 PA (GUNT/) GUNTHER E.
 PA (MILL/) MILLET I.
 PA (SCIO/) SCIORE P.
 PA (ELLE/) ELLERMAN K.
 PA (MACD/) MACDOUGALL J R.
 PA (SMIT/) SMITHSON G.
 Query Match
 Best Local Similarity 11.7%; Score 54; DB 7; Length 5636;
 RESULT 1403
 ID ADK60205 standard; protein; 5636 AA.
 DE Angiogenesis differentially expressed protein GS-P29.
 PN FR2836687-A1.
 PD 05-SEP-2003.
 PA (GENE-) GENE SIGNAL.
 PA (ALMA/) AL MAHMOOD S.

Query Match
Best Local Similarity 11.7%; Score 54; DB 8; Length 5636;
RESULT 1404
ID AUK60506 standard; protein; 5636 AA.
DE Angiogenesis differentially expressed protein GS-P29.
PN FR2836686-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match
Best Local Similarity 11.7%; Score 54; DB 8; Length 5636;
RESULT 1405
ID ADP73129 standard; protein; 5636 AA.
DE Angiogenesis inhibitor human protein sequence, GS-P29.
PN FR2843753-A1.
PD 27-FEB-2004.
PA (GENE/) GENE S.
PA (ALMS/) AL M S.
Query Match
Best Local Similarity 11.7%; Score 54; DB 8; Length 5636;
RESULT 1406
ID AAU65897 standard; protein; 74 AA.
DE Propionibacterium acnes immunogenic protein #26793.
PN W0200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 11.6%; Score 53.5; DB 4; Length 74;
RESULT 1407
ID AEM62416 standard; protein; 74 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #27092.
PN W02003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 11.6%; Score 53.5; DB 6; Length 74;
RESULT 1408
ID ABP11011 standard; protein; 77 AA.
DE Human ORFX protein sequence SEQ ID NO:22004.
PN W0200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 11.6%; Score 53.5; DB 5; Length 77;
RESULT 1409
ID A8054186 standard; protein; 79 AA.
DE Human genome derived single exon protein #420.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match
Best Local Similarity 11.6%; Score 53.5; DB 8; Length 79;
RESULT 1410
ID ADF61855 standard; protein; 115 AA.
DE G3-2H6 protein which is derived from DNA antisense to human DDX9 DNA.
PN W02003088910-A2.
PD 30-OCT-2003.
PA (RIGE-) RIGEL PHARM INC.
Query Match
Best Local Similarity 11.6%; Score 53.5; DB 7; Length 115;
RESULT 1411
ID ADD28235 standard; protein; 135 AA.
DE Human heterodimeric antibody heavy chain variable region SEQ ID NO:13.
PN W02003076568-A2.
PD 18-SEP-2003.
PA (ALEX-) ALEXION PHARM INC.
Query Match
Best Local Similarity 11.6%; Score 53.5; DB 7; Length 135;
RESULT 1412
ID ADD28318 standard; protein; 135 AA.
DE Human heterodimeric antibody heavy chain variable region SEQ ID NO:96.

PN W02003076568-A2.
PD 18-SEP-2003.
PA (ALEX-) ALEXION PHARM INC.
Query Match
Best Local Similarity 11.6%; Score 53.5; DB 7; Length 135;
RESULT 1413
ID ADF07091 standard; protein; 143 AA.
DE Bacterial polypeptide #3204.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 11.6%; Score 53.5; DB 7; Length 143;
RESULT 1414
ID AAB95410 standard; protein; 152 AA.
DE Human protein sequence SEQ ID NO:17796.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 11.6%; Score 53.5; DB 4; Length 152;
RESULT 1415
ID AAM48371 standard; protein; 152 AA.
DE Human SP24 protein.
PN CN1323803-A.
PD 28-NOV-2001.
PA (SHAN-) SHANGHAI CITY INST ONCOLOGY.
Query Match
Best Local Similarity 11.6%; Score 53.5; DB 5; Length 152;
RESULT 1416
ID ADK60188 standard; protein; 152 AA.
DE Angiogenesis differentially expressed protein GS-P11.
PN FR2836687-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match
Best Local Similarity 11.6%; Score 53.5; DB 8; Length 152;
RESULT 1417
ID ADK60489 standard; protein; 152 AA.
DE Angiogenesis differentially expressed protein GS-P11.
PN FR2836686-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match
Best Local Similarity 11.6%; Score 53.5; DB 8; Length 152;
RESULT 1418
ID ADP73112 standard; protein; 152 AA.
DE Angiogenesis inhibitor human protein sequence, GS-P11.
PN FR2843753-A1.
PD 27-FEB-2004.
PA (GENE/) GENE S.
PA (ALMS/) AL M S.
Query Match
Best Local Similarity 11.6%; Score 53.5; DB 8; Length 152;
RESULT 1419
ID ABB97583 standard; protein; 157 AA.
DE Novel human protein SEQ ID NO: 851.
PN W0200222660-A2.
PD 21-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 11.6%; Score 53.5; DB 5; Length 157;
RESULT 1420
ID ADF05894 standard; protein; 162 AA.
DE Bacterial polypeptide #2007.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 11.6%; Score 53.5; DB 7; Length 162;
RESULT 1421

ID ABG11587 standard; protein; 189 AA.
DE Novel human diagnostic protein #11578.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.6%; Score 53.5; DB 4; Length 189;
Best Local Similarity 22.5%; Pred. No. 6.2e+02;
RESULT 1422
ID AAW93199 standard; protein; 227 AA.
DE Pestivirus Erns cytotoxic polypeptide fragment pErns-bd78.
PN WO9906569-A1.
PD 11-FEB-1999.
PA (DIER-) STICHTING INST DIERHOUDERTJ EN DIERGEZON.
Query Match 11.6%; Score 53.5; DB 2; Length 227;
Best Local Similarity 29.0%; Pred. No. 8.1e+02;
RESULT 1423
ID AAG91824 standard; protein; 229 AA.
DE C glutamicum protein fragment SEQ ID NO: 5578.
PN EP1108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 11.6%; Score 53.5; DB 4; Length 229;
Best Local Similarity 27.5%; Pred. No. 8.2e+02;
RESULT 1424
ID ADM74712 standard; protein; 247 AA.
DE Fusarium oxysporum trypsinogen-like mutant protein - K197*.
PN WO2004029202-A2.
PD 08-APR-2004.
PA (NOVO) NOVOZYMES BIOTECH INC.
Query Match 11.6%; Score 53.5; DB 8; Length 247;
Best Local Similarity 24.7%; Pred. No. 9.1e+02;
RESULT 1425
ID AAB76512 standard; protein; 252 AA.
DE Corynebacterium glutamicum MCT protein SEQ ID NO: 6.
PN WO200100805-A2.
PD 04-JAN-2001.
PA (BADI) BASF AG.
Query Match 11.6%; Score 53.5; DB 4; Length 252;
Best Local Similarity 28.3%; Pred. No. 9.3e+02;
RESULT 1426
ID AAG90689 standard; protein; 252 AA.
DE C glutamicum protein fragment SEQ ID NO: 4443.
PN EP1108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 11.6%; Score 53.5; DB 4; Length 252;
Best Local Similarity 28.3%; Pred. No. 9.3e+02;
RESULT 1427
ID AAO18405 standard; protein; 252 AA.
DE C glutamicum cysQ transporter.
PN DE10057801-A1.
PD 23-MAY-2002.
PA (DEGS) DEGUSSA AG.
Query Match 11.6%; Score 53.5; DB 5; Length 252;
Best Local Similarity 28.3%; Pred. No. 9.3e+02;
RESULT 1428
ID ABP46112 standard; protein; 255 AA.
DE Human Blys binding scFv SEQ ID 2123.
PN WO200202641-A1.
PD 10-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
Query Match 11.6%; Score 53.5; DB 5; Length 255;
Best Local Similarity 30.1%; Pred. No. 9.5e+02;
RESULT 1429
ID ADG96939 standard; protein; 255 AA.
DE Single chain antibody that immunospecifically binds Blys SeqID 2123.
PN WO2003055979-A2.
PD 10-JUL-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.6%; Score 53.5; DB 7; Length 255;
Best Local Similarity 30.1%; Pred. No. 9.5e+02;
RESULT 1430
ID ABU50707 standard; protein; 272 AA.
DE Helicobacter pylori selected interacting domain (SID) protein #50.
PN WO200266501-A2.
PD 29-AUG-2002.
PA (HYBR-) HYBRIGENICS.
PA (INSP) INST PASTEUR.
Query Match 11.6%; Score 53.5; DB 5; Length 272;
Best Local Similarity 28.8%; Pred. No. 1e+03;
RESULT 1431
ID AAR03560 standard; protein; 275 AA.
DE Human differentially expressed kidney cDNA 22360 encoded protein.
PN WO200141805-A1.
PD 14-JUN-2001.
PA (GENE-) GENE LOGIC INC.
Query Match 11.6%; Score 53.5; DB 4; Length 275;
Best Local Similarity 32.4%; Pred. No. 1.1e+03;
RESULT 1432
ID ADE07990 standard; protein; 280 AA.
DE Novel protein (useful for identifying genetic disorders) #145.
PN WO2003054152-A2.
PD 03-JUN-2003.
PA (HYSE-) HYSEQ INC.
Query Match 11.6%; Score 53.5; DB 7; Length 280;
Best Local Similarity 32.4%; Pred. No. 1.1e+03;
RESULT 1433
ID AAU38415 standard; protein; 281 AA.
DE Salmonella typhi cellular proliferation protein #306.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.6%; Score 53.5; DB 4; Length 281;
Best Local Similarity 30.6%; Pred. No. 1.1e+03;
RESULT 1434
ID AAM29269 standard; protein; 283 AA.
DE Clostridium perfringens mutant epsilon toxin H106X.
PN WO9734001-A1.
PD 18-SEP-1997.
PA (MINA) UK SEC FOR DEFENCE.
Query Match 11.6%; Score 53.5; DB 2; Length 283;
Best Local Similarity 33.3%; Pred. No. 1.1e+03;
RESULT 1435
ID AAU34520 standard; protein; 285 AA.
DE E. coli cellular proliferation protein #101.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.6%; Score 53.5; DB 4; Length 285;
Best Local Similarity 30.6%; Pred. No. 1.1e+03;
RESULT 1436
ID ABU44856 standard; protein; 285 AA.
DE Protein encoded by Prokaryotic essential gene #30383.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.6%; Score 53.5; DB 6; Length 285;
Best Local Similarity 30.6%; Pred. No. 1.1e+03;
RESULT 1437
ID ABU48045 standard; protein; 285 AA.
DE Protein encoded by Prokaryotic essential gene #33572.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.6%; Score 53.5; DB 6; Length 285;
Best Local Similarity 30.6%; Pred. No. 1.1e+03;
RESULT 1438
ID ABU28576 standard; protein; 285 AA.
DE Protein encoded by Prokaryotic essential gene #14103.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.6%; Score 53.5; DB 6; Length 285;
Best Local Similarity 30.6%; Pred. No. 1.1e+03;
RESULT 1439

ID AAY77118 standard; protein; 288 AA.
 DE Ebola virus structural protein VP30#2.
 PN WO200000617-A2.
 PD 06-JAN-2000.
 PA (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
 Query Match 11.6%; Score 53.5; DB 3; Length 288;
 Best Local Similarity 35.8%; Pred. No. 1.1e+03;
 RESULT 1440
 ID ADM99139 standard; protein; 288 AA.
 DE Environmentally sourced protease protein SeqID 22.
 PN WO2004033668-A2.
 PD 22-APR-2004.
 PA (DIVE-) DIVERSA CORP.
 Query Match 11.6%; Score 53.5; DB 8; Length 288;
 Best Local Similarity 21.3%; Pred. No. 1.1e+03;
 RESULT 1441
 ID ABG79184 standard; protein; 321 AA.
 DE Human mas proto-oncogene-like protein.
 PN WO200264791-A2.
 PD 22-AUG-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 11.6%; Score 53.5; DB 5; Length 321;
 Best Local Similarity 25.8%; Pred. No. 1.3e+03;
 RESULT 1442
 ID ADB65166 standard; protein; 325 AA.
 DE Human protein encoded by clone SPLEN20118050.
 PN EPI308459-A2.
 PD 07-MAY-2003.
 PA (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 11.6%; Score 53.5; DB 7; Length 325;
 Best Local Similarity 41.9%; Pred. No. 1.3e+03;
 RESULT 1443
 ID AAM29268 standard; protein; 328 AA.
 DE Clostridium perfringens mutant epsilon toxin SDM10.
 PN WO9734001-A1.
 PD 18-SEP-1997.
 PA (MINA) UK SEC FOR DEFENCE.
 Query Match 11.6%; Score 53.5; DB 2; Length 328;
 Best Local Similarity 33.3%; Pred. No. 1.3e+03;
 RESULT 1444
 ID AAG39794 standard; protein; 344 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 49290.
 PN EPI033405-A2.
 PD 06-SEP-2000.
 Query Match 11.6%; Score 53.5; DB 3; Length 344;
 Best Local Similarity 45.2%; Pred. No. 1.4e+03;
 RESULT 1445
 ID AAG46277 standard; protein; 346 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 58202.
 PN EPI033405-A2.
 PD 06-SEP-2000.
 Query Match 11.6%; Score 53.5; DB 3; Length 346;
 Best Local Similarity 28.0%; Pred. No. 1.5e+03;
 RESULT 1446
 ID AAG41884 standard; protein; 346 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 52167.
 PN EPI033405-A2.
 PD 06-SEP-2000.
 Query Match 11.6%; Score 53.5; DB 3; Length 346;
 Best Local Similarity 28.0%; Pred. No. 1.5e+03;
 RESULT 1447
 ID AAG46276 standard; protein; 353 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 58201.
 PN EPI033405-A2.
 PD 06-SEP-2000.
 Query Match 11.6%; Score 53.5; DB 3; Length 353;
 Best Local Similarity 28.0%; Pred. No. 1.5e+03;
 RESULT 1448
 ID AAG41883 standard; protein; 353 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 52166.
 PN EPI033405-A2.
 PD 06-SEP-2000.

Query Match 11.6%; Score 53.5; DB 3; Length 353;
 Best Local Similarity 28.0%; Pred. No. 1.5e+03;
 RESULT 1449
 ID AAG41882 standard; protein; 355 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 52165.
 PN EPI033405-A2.
 PD 06-SEP-2000.
 Query Match 11.6%; Score 53.5; DB 3; Length 355;
 Best Local Similarity 28.0%; Pred. No. 1.5e+03;
 RESULT 1450
 ID AAG46275 standard; protein; 355 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 58200.
 PN EPI033405-A2.
 PD 06-SEP-2000.
 Query Match 11.6%; Score 53.5; DB 3; Length 355;
 Best Local Similarity 28.0%; Pred. No. 1.5e+03;
 RESULT 1451
 ID AAR05159 standard; protein; 368 AA.
 DE Sequence of human bone proteoglycan I (biglycan).
 PN USN7432044-N.
 PD 17-APR-1990.
 PA (USSH) NAT INST OF HEALTH.
 Query Match 11.6%; Score 53.5; DB 2; Length 368;
 Best Local Similarity 41.9%; Pred. No. 1.6e+03;
 RESULT 1452
 ID AAB85043 standard; protein; 368 AA.
 DE Human biglycan protein sequence.
 PN WO200136475-A2.
 PD 25-MAY-2001.
 PA (UYBR-) UNIV BROWN RES FOUND.
 Query Match 11.6%; Score 53.5; DB 4; Length 368;
 Best Local Similarity 41.9%; Pred. No. 1.6e+03;
 RESULT 1453
 ID AAG78510 standard; protein; 368 AA.
 DE Human biglycan amino acid sequence.
 PN US6277812-B1.
 PD 21-AUG-2001.
 PA (BURN-) BURNHAM INST.
 Query Match 11.6%; Score 53.5; DB 4; Length 368;
 Best Local Similarity 41.9%; Pred. No. 1.6e+03;
 RESULT 1454
 ID AAE34394 standard; protein; 368 AA.
 DE Human biglycan protein.
 PN WO200295415-A2.
 PD 28-NOV-2002.
 PA (OSTE-) OSTEOMETER BIO TECH AS.
 Query Match 11.6%; Score 53.5; DB 6; Length 368;
 Best Local Similarity 41.9%; Pred. No. 1.6e+03;
 RESULT 1455
 ID ABR47399 standard; protein; 368 AA.
 DE Breast cancer associated protein sequence SEQ ID NO:29.
 PN WO2003004989-A2.
 PD 16-JAN-2003.
 PA (MILL-) MILLENIUM PHARM INC.
 Query Match 11.6%; Score 53.5; DB 6; Length 368;
 Best Local Similarity 41.9%; Pred. No. 1.6e+03;
 RESULT 1456
 ID ABR39564 standard; protein; 368 AA.
 DE Human biglycan protein sequence.
 PN WO2003015615-A2.
 PD 27-FEB-2003.
 PA (UYBR-) UNIV BROWN RES FOUND.
 Query Match 11.6%; Score 53.5; DB 6; Length 368;
 Best Local Similarity 41.9%; Pred. No. 1.6e+03;
 RESULT 1457
 ID ADB70376 standard; protein; 368 AA.
 DE Proteoglycan I (biglycan) SEQ ID NO:68.
 PN WO2003012229-A2.
 PD 13-MAR-2003.
 PA (BGMH) BRIGHAM & WOMENS HOSPITAL INC.
 Query Match 11.6%; Score 53.5; DB 7; Length 368;
 Best Local Similarity 41.9%; Pred. No. 1.6e+03;
 RESULT 1458

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ID ABB80259 standard; protein; 368 AA.
 DE Human biglycan.
 PN WO2003070195-A2.
 PD 28-AUG-2003.
 PA (UYBR-) UNIV BROWN RES FOUND.
 Query Match 11.6%; Score 53.5; DB 7; Length 368;
 Best Local Similarity 41.9%; Pred. No. 1.6e+03;
 RESULT 1459
 ID ADD14060 standard; protein; 368 AA.
 DE Human src biomarker polypeptide SEQ ID NO:249.
 PN WO2003062395-A2.
 PD 31-JUL-2003.
 PA (BRIM-) BRISTOL-MYERS SQUIBB CO.
 Query Match 11.6%; Score 53.5; DB 7; Length 368;
 Best Local Similarity 41.9%; Pred. No. 1.6e+03;
 RESULT 1460
 ID ADN95819 standard; protein; 368 AA.
 DE Human REC/LEC-related protein sequence SeqID743.
 PN WO2003080640-A1.
 PD 02-OCT-2003.
 PA (LUDW-) LUDWIG INST CANCER RES.
 PA (LICN-) LICENTIA LTD.
 Query Match 11.6%; Score 53.5; DB 7; Length 368;
 Best Local Similarity 41.9%; Pred. No. 1.6e+03;
 RESULT 1461
 ID ADP65209 standard; protein; 368 AA.
 DE Human biglycan preproprotein, bone/cartilage proteoglycan-I, dermatan.
 PN WO2003072827-A1.
 PD 04-SEP-2003.
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 Query Match 11.6%; Score 53.5; DB 7; Length 368;
 Best Local Similarity 41.9%; Pred. No. 1.6e+03;
 RESULT 1462
 ID ADJ37155 standard; protein; 368 AA.
 DE Human malignant pleural mesothelioma (MPM) protein #30.
 PN US2003219760-A1.
 PD 27-NOV-2003.
 PA (EGEM-) BRIGHAM & WOMENS HOSPITAL INC.
 Query Match 11.6%; Score 53.5; DB 8; Length 368;
 Best Local Similarity 41.9%; Pred. No. 1.6e+03;
 RESULT 1463
 ID ADL09055 standard; protein; 368 AA.
 DE Human biglycan protein.
 PN US2004063627-A1.
 PD 01-APR-2004.
 PA (FALL-) FALLON J R.
 PA (MCKE-) MCKECHNIE B.
 PA (RAFI-) RAFI M.
 PA (CREE-) CREELEY H.
 PA (BOWE-) BOWE M A.
 PA (FERR-) FERRI R.
 Query Match 11.6%; Score 53.5; DB 8; Length 368;
 Best Local Similarity 41.9%; Pred. No. 1.6e+03;
 RESULT 1464
 ID ADO28665 standard; protein; 368 AA.
 DE Human PGS1 protein SEQ ID NO:94.
 PN WO2004044178-A2.
 PD 27-MAY-2004.
 PA (GETH-) GENENTECH INC.
 Query Match 11.6%; Score 53.5; DB 8; Length 368;
 Best Local Similarity 41.9%; Pred. No. 1.6e+03;
 RESULT 1465
 ID ADP81182 standard; protein; 410 AA.
 DE Protein of human ovarian specific gene, SEQ ID NO 216.
 PN WO2004053079-A2.
 PD 24-JUN-2004.
 PA (DIAD-) DIADEXUS INC.
 Query Match 11.6%; Score 53.5; DB 8; Length 410;
 Best Local Similarity 25.0%; Pred. No. 1.8e+03;
 RESULT 1466
 ID AAG39793 standard; protein; 411 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 49289.
 PN EP1033405-A2.

PD 06-SEP-2000.
 Query Match 11.6%; Score 53.5; DB 3; Length 411;
 Best Local Similarity 45.2%; Pred. No. 1.9e+03;
 RESULT 1467
 ID AAU30348 standard; protein; 423 AA.
 DE Novel human secreted protein #839.
 PN WO200179449-A2.
 PD 25-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 11.6%; Score 53.5; DB 4; Length 423;
 Best Local Similarity 41.9%; Pred. No. 1.9e+03;
 RESULT 1468
 ID ADF05084 standard; protein; 432 AA.
 DE Bacterial polypeptide #1197.
 PN US6605709-B1.
 PD 12-AUG-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 11.6%; Score 53.5; DB 7; Length 432;
 Best Local Similarity 22.4%; Pred. No. 2e+03;
 RESULT 1469
 ID ABB65759 standard; protein; 436 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 24069.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEXE-) PE CORP NY.
 Query Match 11.6%; Score 53.5; DB 4; Length 436;
 Best Local Similarity 30.3%; Pred. No. 2e+03;
 RESULT 1470
 ID ADJ67556 standard; protein; 447 AA.
 DE Human ovarian specific polypeptide SEQ ID NO:270.
 PN WO2004013111-A2.
 PD 12-FEB-2004.
 PA (DIAD-) DIADEXUS INC.
 Query Match 11.6%; Score 53.5; DB 8; Length 447;
 Best Local Similarity 25.0%; Pred. No. 2.1e+03;
 RESULT 1471
 ID ABU35686 standard; protein; 449 AA.
 DE Protein encoded by Prokaryotic essential gene #21213.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 11.6%; Score 53.5; DB 6; Length 449;
 Best Local Similarity 35.7%; Pred. No. 2.1e+03;
 RESULT 1472
 ID AAU76413 standard; protein; 450 AA.
 DE Dimethylallyltryptophan synthase (DmaW) version #2.
 PN US6335188-B1.
 PD 01-JAN-2002.
 PA (KENT-) UNIV KENTUCKY RES FOUND.
 Query Match 11.6%; Score 53.5; DB 5; Length 450;
 Best Local Similarity 31.7%; Pred. No. 2.1e+03;
 RESULT 1473
 ID AAG39792 standard; protein; 452 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 49288.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 11.6%; Score 53.5; DB 3; Length 452;
 Best Local Similarity 45.2%; Pred. No. 2.1e+03;
 RESULT 1474
 ID ABP38702 standard; protein; 454 AA.
 DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3547.
 PN US6380370-B1.
 PD 30-APR-2002.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 11.6%; Score 53.5; DB 5; Length 454;
 Best Local Similarity 24.4%; Pred. No. 2.1e+03;
 RESULT 1475
 ID ABO67616 standard; protein; 455 AA.
 DE Klebsiella pneumoniae polypeptide seqid 14133.
 PN US6610836-B1.
 PD 26-AUG-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 11.6%; Score 53.5; DB 7; Length 455;

Best Local Similarity 22.4%; Pred. No. 2.1e+03;
RESULT 1476
ID AAW05754 standard; protein; 467 AA.
DE Presentilin-1-1 A285V mutation.
PN W09634099-A2.
PD 31-OCT-1996.
PA (HSCR-) HSC RES & DEV LP.
PA (UTOR-) UNIV TORONTO GOVERNING COUNCIL.
Query Match 11.6%; Score 53.5; DB 2; Length 467;
Best Local Similarity 19.4%; Pred. No. 2.2e+03;
RESULT 1477
ID AD808682 standard; protein; 477 AA.
DE Novel protein (useful for identifying genetic disorders) #837.
PN W02003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 11.6%; Score 53.5; DB 7; Length 477;
Best Local Similarity 32.4%; Pred. No. 2.3e+03;
RESULT 1478
ID ADN99232 standard; protein; 477 AA.
DE Novel human protein sequence #48.
PN W02004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 11.6%; Score 53.5; DB 8; Length 477;
Best Local Similarity 32.4%; Pred. No. 2.3e+03;
RESULT 1479
ID ADP81186 standard; protein; 481 AA.
DE Protein of human ovarian specific gene, SEQ ID No 220.
PN W02004053079-A2.
PD 24-JUN-2004.
PA (DIAD-) DIADEXUS INC.
Query Match 11.6%; Score 53.5; DB 8; Length 481;
Best Local Similarity 25.0%; Pred. No. 2.3e+03;
RESULT 1480
ID ABP54055 standard; protein; 487 AA.
DE Streptococcus pneumoniae MEL mega ORF2 protein SEQ ID NO:3.
PN W0200277196-A2.
PD 03-OCT-2002.
PA (UYEM-) UNIV EMORY.
Query Match 11.6%; Score 53.5; DB 6; Length 487;
Best Local Similarity 17.7%; Pred. No. 2.3e+03;
RESULT 1481
ID ADD69366 standard; protein; 503 AA.
DE Human Ang-4 protein - SEQ ID 102.
PN W02003048185-A2.
PD 12-JUN-2003.
PA (GENV-) GENVEC INC.
Query Match 11.6%; Score 53.5; DB 7; Length 503;
Best Local Similarity 27.7%; Pred. No. 2.5e+03;
RESULT 1482
ID ABU50821 standard; protein; 504 AA.
DE Helicobacter pylori selected interacting domain (SID) protein #164.
PN W0200266501-A2.
PD 29-AUG-2002.
PA (HYBR-) HYBRIGENICS.
PA (INSP-) INST PASTEUR.
Query Match 11.6%; Score 53.5; DB 5; Length 504;
Best Local Similarity 28.8%; Pred. No. 2.5e+03;
RESULT 1483
ID AAO24288 standard; protein; 509 AA.
DE H pylori motility associated flaA protein.
PN W02003080654-A2.
PD 02-OCT-2003.
PA (CANA-) NAT RES COUNCIL CANADA.
Query Match 11.6%; Score 53.5; DB 7; Length 509;
Best Local Similarity 28.8%; Pred. No. 2.5e+03;
RESULT 1484
ID AAW61269 standard; protein; 510 AA.
DE Helicobacter pylori flagellin FlaA.
PN W09823288-A1.
PD 04-JUN-1998.
PA (ASTR-) ASTRA AB.
Query Match 11.6%; Score 53.5; DB 2; Length 510;
Best Local Similarity 28.8%; Pred. No. 2.5e+03;
RESULT 1485
ID ABB54776 standard; protein; 517 AA.
DE Lactococcus lactis protein kinB.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG-) INRA INST NAT RECH AGRONOMIQUE.
Query Match 11.6%; Score 53.5; DB 5; Length 517;
Best Local Similarity 25.8%; Pred. No. 2.6e+03;
RESULT 1486
ID ABB49086 standard; protein; 558 AA.
DE Listeria monocytogenes protein #1790.
PN W0200177335-A2.
PD 18-OCT-2001.
PA (INSP-) INST PASTEUR.
Query Match 11.6%; Score 53.5; DB 5; Length 558;
Best Local Similarity 31.5%; Pred. No. 2.8e+03;
RESULT 1487
ID ABG18722 standard; protein; 560 AA.
DE Novel human diagnostic protein #18713.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.6%; Score 53.5; DB 4; Length 560;
Best Local Similarity 28.3%; Pred. No. 2.9e+03;
RESULT 1488
ID AAY49634 standard; protein; 571 AA.
DE Human sdph3.10 (SAGE) protein.
PN W09953061-A2.
PD 21-OCT-1999.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match 11.6%; Score 53.5; DB 2; Length 571;
Best Local Similarity 36.4%; Pred. No. 2.9e+03;
RESULT 1489
ID AAY58040 standard; protein; 579 AA.
DE Rhodobacter sphaeroides phaC synthase protein sequence.
PN JP11239492-A.
PD 02-NOV-1999.
PA (CHIK-) ZH CHIKYU KANKYO SANGYO GIJITSU KENKYU.
PA (ENIE-) ENITECNOLOGIE SPA.
Query Match 11.6%; Score 53.5; DB 3; Length 579;
Best Local Similarity 19.1%; Pred. No. 3e+03;
RESULT 1490
ID AAB23034 standard; protein; 590 AA.
DE Human SLIT protein-like splice variant, SECX 3352358-2.
PN W0200053742-A2.
PD 14-SEP-2000.
PA (CURA-) CURAGEN CORP.
Query Match 11.6%; Score 53.5; DB 3; Length 590;
Best Local Similarity 31.4%; Pred. No. 3.1e+03;
RESULT 1491
ID ADA23289 standard; protein; 590 AA.
DE Human SECX polypeptide, SEC6.
PN US2003054514-A1.
PD 20-MAR-2003.
PA (SHIM/) SHIMKETS R A.
PA (LARO/) LAROCHELLE W J.
Query Match 11.6%; Score 53.5; DB 6; Length 590;
Best Local Similarity 31.4%; Pred. No. 3.1e+03;
RESULT 1492
ID AAE10894 standard; protein; 601 AA.
DE Rhodobacter sphaeroides polyhydroxybutyrate (PHB) synthase.
PN W0200164897-A2.
PD 07-SEP-2001.
PA (KELC-) CP KELCO US INC.
Query Match 11.6%; Score 53.5; DB 4; Length 601;
Best Local Similarity 19.1%; Pred. No. 3.2e+03;
RESULT 1493
ID ABB88993 standard; protein; 613 AA.
DE Babesia microti antigen BM-12.
PN W0200185947-A2.
PD 15-NOV-2001.

PA (CORI-) CORIXA CORP.
 Query Match 11.6%; Score 53.5; DB 5; Length 613;
 Best Local Similarity 32.7%; Pred. No. 3.2e+03;
 RESULT 1494
 ID ADE06121 standard; protein; 613 AA.
 DE BMNI-related polypeptide #55.
 PN US2003109689-A1.
 PD 12-JUN-2003.
 PA (REED/) REED S G.
 PA (LODE/) LODES M J.
 PA (HOUG/) HOUGHTON R L.
 PA (SLEA/) SLEATH P R.
 PA (MCNE/) MCNEILL P D.
 PA (HOME/) HOMER M J.
 PA (SECR/) SECRIST H.
 Query Match 11.6%; Score 53.5; DB 7; Length 613;
 Best Local Similarity 32.7%; Pred. No. 3.2e+03;
 RESULT 1495
 ID ADN01966 standard; protein; 632 AA.
 DE Staphylococcus aureus related bacteriophage protein #15.
 PN WO2004020635-A1.
 PD 11-MAR-2004.
 PA (TECH-) TECHNO NETWORK SHIKOKU CO LTD.
 Query Match 11.6%; Score 53.5; DB 8; Length 632;
 Best Local Similarity 25.6%; Pred. No. 3.4e+03;
 RESULT 1496
 ID ADA23287 standard; protein; 653 AA.
 DE Human SECX polypeptide, SEC5 #1.
 PN US2003054514-A1.
 PD 20-MAR-2003.
 PA (SHIM/) SHIMKETS R A.
 PA (LARO/) LAROCHELLE W J.
 Query Match 11.6%; Score 53.5; DB 6; Length 653;
 Best Local Similarity 31.4%; Pred. No. 3.5e+03;
 RESULT 1497
 ID ADE08480 standard; protein; 661 AA.
 DE Novel protein (useful for identifying genetic disorders) #635.
 PN WO2003054152-A2.
 PD 03-JUL-2003.
 PA (HYSE-) HYSEQ INC.
 Query Match 11.6%; Score 53.5; DB 7; Length 661;
 Best Local Similarity 41.9%; Pred. No. 3.6e+03;
 RESULT 1498
 ID AAY94754 standard; protein; 687 AA.
 DE Protein encoded by yeast essential gene SSY5.
 PN WO200058457-A2.
 PD 05-OCT-2000.
 PA (ROSE-) ROSETTA INPHARMATICS INC.
 Query Match 11.6%; Score 53.5; DB 3; Length 687;
 Best Local Similarity 31.5%; Pred. No. 3.8e+03;
 RESULT 1499
 ID AAB23033 standard; protein; 694 AA.
 DE Human SLIT protein-like splice variant, SECX 3352358-1.
 PN WO200053742-A2.
 PD 14-SEP-2000.
 PA (CURA-) CURAGEN CORP.
 Query Match 11.6%; Score 53.5; DB 3; Length 694;
 Best Local Similarity 31.4%; Pred. No. 3.9e+03;
 RESULT 1500
 ID ABG08646 standard; protein; 696 AA.
 DE Novel human diagnostic protein #8637.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 11.6%; Score 53.5; DB 4; Length 696;
 Best Local Similarity 28.9%; Pred. No. 3.9e+03;